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APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO./TITLE
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09/001,737 12/31/97 MIZZEN

L 870109.408

0252/0414

SEED AND BERRY  
6300 COLUMBIA CENTER  
701 FIFTH AVENUE  
SEATTLE WA 98104-7092

NOT ASSIGNED

1643

DATE MAILED:

04/14/98

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS  
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application fails to comply with the requirements of 37 CFR 1.821 - 1.825.
- ☒ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- ☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.832, as indicated on the attached marked-up copy of the "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).
- ☐ 7. OTHER:

**APPLICANT MUST PROVIDE:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing."
- ☒ An initial or substitute paper copy of the "Sequence Listing," as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b) or 1.825(d).

**FOR QUESTIONS REGARDING COMPLIANCE WITH THESE REQUIREMENTS, PLEASE CONTACT:**

- ☐ For Rules Interpretation, call (703) 308-1123.
- ☒ For CRF submission help, call (703) 308-4212.
- ☐ For PatentIn software help, call (703) 308-6856.

*[Signature]*  
Customer Service Center  
Initial/Patent Examination Division (703) 308-1202



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Mizzen, Lee  
Wisniewski, Jan
- (ii) TITLE OF INVENTION: STREPTOCACCAL HEAT SHOCK PROTEINS OF THE  
HSP60 FAMILY
- (iii) NUMBER OF SEQUENCES: 91
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: SEED and BERRY LLP
  - (B) STREET: 701 Fifth Avenue, 6300 Columbia Center
  - (C) CITY: Seattle
  - (D) STATE: Washington
  - (E) COUNTRY: USA
  - (F) ZIP: 98104
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 09/001,737
  - (B) FILING DATE: 31-DEC-1997
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Sharkey, Richard G.
  - (B) REGISTRATION NUMBER: 32,629
  - (C) REFERENCE/DOCKET NUMBER: 870109.408
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (206) 622-4900
  - (B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1665 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 15..1649
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCT TCAT	ATG GCG GCT AAA GAC GTA AAA TTC GGT AAC GAC GCT	50
	Met Ala Ala Lys Asp Val Lys Phe Gly Asn Asp Ala	
	1 5 10	
CGT GTG AAA ATG CTG CGC GGC GTA AAC GTA CTG GCA GAT GCA GTG AAA		98
Arg Val Lys Met Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys		
	15 20 25	
GTT ACC CTC GGC CCA AAA GGC CGT AAC GTA GTT CTG GAT AAA TCT TTC		146
Val Thr Leu Gly Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe		
	30 35 40	
GGT GCA CCG ACC ATC ACT AAA GAT GGT GTT TCC GTA GCA CGT GAA ATC		194
Gly Ala Pro Thr Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile		
	45 50 55 60	
GAA CTG GAA GAC AAG TTC GAA AAC ATG GGT GCG CAG ATG GTG AAA GAA		242
Glu Leu Glu Asp Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu		
	65 70 75	
GTT GCC TCT AAA GCG AAC GAC GCT GCA GGT GAC GGT ACC ACC ACC GCA		290
Val Ala Ser Lys Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala		
	80 85 90	
ACC GTA CTG GCT CAG TCC ATC ATC ACT GAA GGC CTG AAA GCC GTT GCT		338
Thr Val Leu Ala Gln Ser Ile Ile Thr Glu Gly Leu Lys Ala Val Ala		
	95 100 105	
GCG GGC ATG AAC CCG ATG GAT CTG AAA CGT GGT ATC GAC AAA GCT GTC		386
Ala Gly Met Asn Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val		
	110 115 120	
GCT GCT GCT GTT GAA GAA CTG AAA GCA CTG TCC GTA CCG TGC TCC GAC		434
Ala Ala Ala Val Glu Glu Leu Lys Ala Leu Ser Val Pro Cys Ser Asp		
	125 130 135 140	
TCT AAA GCT ATT GCT CAG GTT GGT ACC ATC TCC GCT AAC TCC GAC GAA		482
Ser Lys Ala Ile Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu		
	145 150 155	
ACC GTA GGT AAA CTG ATC GCT GAA GCG ATG GAC AAA GTC GGT AAA GAA		530
Thr Val Gly Lys Leu Ile Ala Glu Ala Met Asp Lys Val Gly Lys Glu		
	160 165 170	
GGC GTG ATC ACC GTT GAA GAC GGT ACC GGT CTG CAG GAC GAA CTG GAC		578
Gly Val Ile Thr Val Glu Asp Gly Thr Gly Leu Gln Asp Glu Leu Asp		
	175 180 185	
GTG GTT GAA GGT ATG CAG TTC GAC CGT GGC TAC CTG TCT CCT TAC TTC		626
Val Val Glu Gly Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe		
	190 195 200	
ATC AAC AAG CCG GAA ACT GGC GCA GTA GAA TTG GAA AGC CCG TTC ATC		674
Ile Asn Lys Pro Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile		
	205 210 215 220	
CTG CTG GCT GAC AAG AAA ATC TCC AAC ATC CGC GAA ATG CTG CCG GTT		722

Leu	Leu	Ala	Asp	Lys	Lys	Ile	Ser	Asn	Ile	Arg	Glu	Met	Leu	Pro	Val	
				225					230					235		
CTG	GAA	GCT	GTA	GCG	AAA	GCA	GGC	AAA	CCG	CTG	CTG	ATC	ATC	GCT	GAA	770
Leu	Glu	Ala	Val	Ala	Lys	Ala	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	
			240					245					250			
GAT	GTT	GAA	GGC	GAA	GCG	CTG	GCA	ACT	CTG	GTT	GTT	AAC	ACC	ATG	CGC	818
Asp	Val	Glu	Gly	Glu	Ala	Leu	Ala	Thr	Leu	Val	Val	Asn	Thr	Met	Arg	
		255					260					265				
GGT	ATC	GTA	AAA	GTC	GCT	GCG	GTT	AAA	GCA	CCT	GGC	TTC	GGC	GAT	CGT	866
Gly	Ile	Val	Lys	Val	Ala	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	
	270					275					280					
CGT	AAA	GCA	ATG	CTG	CAG	GAT	ATC	GCT	ACC	CTG	ACC	GGT	GGT	ACC	GTT	914
Arg	Lys	Ala	Met	Leu	Gln	Asp	Ile	Ala	Thr	Leu	Thr	Gly	Gly	Thr	Val	
285					290					295					300	
ATC	TCT	GAA	GAG	ATC	GGT	ATG	GAG	CTG	GAA	AAA	GCA	ACT	CTG	GAA	GAT	962
Ile	Ser	Glu	Glu	Ile	Gly	Met	Glu	Leu	Glu	Lys	Ala	Thr	Leu	Glu	Asp	
				305					310					315		
CTG	GGC	CAG	GCG	AAA	CGC	GTT	GTT	ATC	AAC	AAA	GAT	ACC	ACC	ACC	ATC	1010
Leu	Gly	Gln	Ala	Lys	Arg	Val	Val	Ile	Asn	Lys	Asp	Thr	Thr	Thr	Ile	
			320					325					330			
ATC	GAT	GGC	GTG	GGC	GAC	GAA	GCT	GCA	ATC	CAG	GGT	CGC	GTG	ACT	CAG	1058
Ile	Asp	Gly	Val	Gly	Asp	Glu	Ala	Ala	Ile	Gln	Gly	Arg	Val	Thr	Gln	
		335					340					345				
ATT	CGT	CAG	CAG	ATC	GAA	GAA	GCA	ACT	TCC	GAC	TAT	GAC	CGT	GAA	AAA	1106
Ile	Arg	Gln	Gln	Ile	Glu	Glu	Ala	Thr	Ser	Asp	Tyr	Asp	Arg	Glu	Lys	
	350					355					360					
CTG	CAG	GAG	CGC	GTA	GCG	AAA	CTG	GCA	GGC	GGC	GTT	GCG	GTT	ATC	AAA	1154
Leu	Gln	Glu	Arg	Val	Ala	Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	
365					370					375					380	
GTT	GGT	GCT	GCG	ACT	GAA	GTT	GAA	ATG	AAA	GAG	AAG	AAA	GCC	CGC	GTT	1202
Val	Gly	Ala	Ala	Thr	Glu	Val	Glu	Met	Lys	Glu	Lys	Lys	Ala	Arg	Val	
				385					390					395		
GAA	GAT	GCC	CTG	CAC	GCT	ACC	CGT	GCT	GCG	GTA	GAA	GAA	GGC	GTG	GTT	1250
Glu	Asp	Ala	Leu	His	Ala	Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	Val	Val	
			400					405					410			
GCT	GGT	GGT	GGC	GTT	GCG	CTG	ATT	CGC	GTA	GCG	TCT	AAA	ATT	GCC	GGC	1298
Ala	Gly	Gly	Gly	Val	Ala	Leu	Ile	Arg	Val	Ala	Ser	Lys	Ile	Ala	Gly	
		415					420					425				
CTG	AAA	GGT	CAG	AAC	GAA	GAC	CAG	AAC	GTA	GGT	ATC	AAA	GTT	GCG	CTG	1346
Leu	Lys	Gly	Gln	Asn	Glu	Asp	Gln	Asn	Val	Gly	Ile	Lys	Val	Ala	Leu	
	430					435					440					
CGC	GCA	ATG	GAA	TCC	CCA	CTG	CGT	CAA	ATC	GTA	CTG	AAC	TGC	GGC	GAA	1394
Arg	Ala	Met	Glu	Ser	Pro	Leu	Arg	Gln	Ile	Val	Leu	Asn	Cys	Gly	Glu	
445					450					455					460	

GAG CCG TCT GTA GTG GCT AAC ACC GTG AAA GCC GGT GAC GGT AAC TAC	1442
Glu Pro Ser Val Val Ala Asn Thr Val Lys Ala Gly Asp Gly Asn Tyr	
465 470 475	
GGT TAC AAC GCT GCA ACT GAA GAA TAC GGC AAC ATG ATC GAC ATG GGT	1490
Gly Tyr Asn Ala Ala Thr Glu Glu Tyr Gly Asn Met Ile Asp Met Gly	
480 485 490	
ATC CTG GAT CCA ACC AAA GTA ACT CGT TCT GCT CTG CAG TAC GCG GCT	1538
Ile Leu Asp Pro Thr Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala	
495 500 505	
TCT GTT GCG GGT CTG ATG ATC ACC ACC GAG TGC ATG GTT ACC GAC CTG	1586
Ser Val Ala Gly Leu Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu	
510 515 520	
CCG AAA GGC GAT GCA CCT GAC TTA GGT GCT GCT GGT GGT ATG GGC GGC	1634
Pro Lys Gly Asp Ala Pro Asp Leu Gly Ala Ala Gly Gly Met Gly Gly	
525 530 535 540	
ATG GGC GGA ATG ATG TGATCAAGCC GAATTC	1665
Met Gly Gly Met Met	
545	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ala Lys Asp Val Lys Phe Gly Asn Asp Ala Arg Val Lys Met	
1 5 10 15	
Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys Val Thr Leu Gly	
20 25 30	
Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr	
35 40 45	
Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp	
50 55 60	
Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys	
65 70 75 80	
Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala	
85 90 95	
Gln Ser Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn	
100 105 110	

Pro	Met	Asp	Leu	Lys	Arg	Gly	Ile	Asp	Lys	Ala	Val	Ala	Ala	Ala	Val	115	120	125
Glu	Glu	Leu	Lys	Ala	Leu	Ser	Val	Pro	Cys	Ser	Asp	Ser	Lys	Ala	Ile	130	135	140
Ala	Gln	Val	Gly	Thr	Ile	Ser	Ala	Asn	Ser	Asp	Glu	Thr	Val	Gly	Lys	145	150	155
Leu	Ile	Ala	Glu	Ala	Met	Asp	Lys	Val	Gly	Lys	Glu	Gly	Val	Ile	Thr	165	170	175
Val	Glu	Asp	Gly	Thr	Gly	Leu	Gln	Asp	Glu	Leu	Asp	Val	Val	Glu	Gly	180	185	190
Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro	Tyr	Phe	Ile	Asn	Lys	Pro	195	200	205
Glu	Thr	Gly	Ala	Val	Glu	Leu	Glu	Ser	Pro	Phe	Ile	Leu	Leu	Ala	Asp	210	215	220
Lys	Lys	Ile	Ser	Asn	Ile	Arg	Glu	Met	Leu	Pro	Val	Leu	Glu	Ala	Val	225	230	235
Ala	Lys	Ala	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	245	250	255
Glu	Ala	Leu	Ala	Thr	Leu	Val	Val	Asn	Thr	Met	Arg	Gly	Ile	Val	Lys	260	265	270
Val	Ala	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Met	275	280	285
Leu	Gln	Asp	Ile	Ala	Thr	Leu	Thr	Gly	Gly	Thr	Val	Ile	Ser	Glu	Glu	290	295	300
Ile	Gly	Met	Glu	Leu	Glu	Lys	Ala	Thr	Leu	Glu	Asp	Leu	Gly	Gln	Ala	305	310	315
Lys	Arg	Val	Val	Ile	Asn	Lys	Asp	Thr	Thr	Thr	Ile	Ile	Asp	Gly	Val	325	330	335
Gly	Asp	Glu	Ala	Ala	Ile	Gln	Gly	Arg	Val	Thr	Gln	Ile	Arg	Gln	Gln	340	345	350
Ile	Glu	Glu	Ala	Thr	Ser	Asp	Tyr	Asp	Arg	Glu	Lys	Leu	Gln	Glu	Arg	355	360	365
Val	Ala	Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	Ala	Ala	370	375	380
Thr	Glu	Val	Glu	Met	Lys	Glu	Lys	Lys	Ala	Arg	Val	Glu	Asp	Ala	Leu	385	390	395
His	Ala	Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	Val	Val	Ala	Gly	Gly	Gly	405	410	415
Val	Ala	Leu	Ile	Arg	Val	Ala	Ser	Lys	Ile	Ala	Gly	Leu	Lys	Gly	Gln			

420	425	430
Asn Glu Asp Gln Asn Val Gly Ile Lys Val Ala Leu Arg Ala Met Glu		
435	440	445
Ser Pro Leu Arg Gln Ile Val Leu Ash Cys Gly Glu Glu Pro Ser Val		
450	455	460
Val Ala Asn Thr Val Lys Ala Gly Asp Gly Asn Tyr Gly Tyr Asn Ala		
465	470	475
Ala Thr Glu Glu Tyr Gly Asn Met Ile Asp Met Gly Ile Leu Asp Pro		
485	490	495
Thr Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala Ser Val Ala Gly		
500	505	510
Leu Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu Pro Lys Gly Asp		
515	520	525
Ala Pro Asp Leu Gly Ala Ala Gly Gly Met Gly Gly Met Gly Gly Met		
530	535	540
Met		
545		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 15..1637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCGGCT TCAT ATG GCA AAA GAA ATT AAA TTT TCA TCA GAT GCC CGT	50
Met Ala Lys Glu Ile Lys Phe Ser Ser Asp Ala Arg	
1 5 10	
TCA GCT ATG GTC CGT GGT GTC GAT ATC CTT GCA GAT ACT GTT AAA GTA	98
Ser Ala Met Val Arg Gly Val Asp Ile Leu Ala Asp Thr Val Lys Val	
15 20 25	
ACT TTG GGA CCA AAA GGT CGC AAT GTC GTT CTT GAA AAG TCA TTC GGT	146
Thr Leu Gly Pro Lys Gly Arg Asn Val Val Leu Glu Lys Ser Phe Gly	
30 35 40	
TCA CCC TTG ATT ACC AAT GAC GGT GTG ACT ATT GCC AAA GAA ATT GAA	194
Ser Pro Leu Ile Thr Asn Asp Gly Val Thr Ile Ala Lys Glu Ile Glu	
45 50 55 60	

TTA GAA GAC CAT TTT GAA AAT ATG GGT GCC AAA TTG GTA TCA GAA GTA Leu Glu Asp His Phe Glu Asn Met Gly Ala Lys Leu Val Ser Glu Val 65 70 75	242
GCT TCA AAA ACC AAT GAT ATC GCA GGT GAT GGA ACT ACA ACT GCA ACT Ala Ser Lys Thr Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr 80 85 90	290
GTT TTG ACC CAA GCA ATC GTC CGT GAA GGA ATC AAA AAC GTC ACA GCA Val Leu Thr Gln Ala Ile Val Arg Glu Gly Ile Lys Asn Val Thr Ala 95 100 105	338
GGT GCA AAT CCA ATC GGT ATT CGT CGT GGG ATT GAA ACA GCA GTT GCC Gly Ala Asn Pro Ile Gly Ile Arg Arg Gly Ile Glu Thr Ala Val Ala 110 115 120	386
GCA GCA GTT GAA GCT TTG AAA AAC AAC GTC ATC CCT GTT GCC AAT AAA Ala Ala Val Glu Ala Leu Lys Asn Asn Val Ile Pro Val Ala Asn Lys 125 130 135 140	434
GAA GCT ATC GCT CAA GTT GCA GCC GTA TCT TCT CGT TCT GAA AAA GTT Glu Ala Ile Ala Gln Val Ala Ala Val Ser Ser Arg Ser Glu Lys Val 145 150 155	482
GGT GAG TAC ATC TCT GAA GCA ATG GAA AAA GTT GGC AAA GAC GGT GTC Gly Glu Tyr Ile Ser Glu Ala Met Glu Lys Val Gly Lys Asp Gly Val 160 165 170	530
ATC ACC ATC GAA GAG TCA CGT GGT ATG GAA ACA GAG CTT GAA GTC GTA Ile Thr Ile Glu Glu Ser Arg Gly Met Glu Thr Glu Leu Glu Val Val 175 180 185	578
GAA GGA ATG CAG TTT GAC CGT GGT TAC CTT TCA CAG TAC ATG GTG ACA Glu Gly Met Gln Phe Asp Arg Gly Tyr Leu Ser Gln Tyr Met Val Thr 190 195 200	626
GAT AGC GAA AAA ATG GTG GCT GAC CTT GAA AAT CCG TAC ATT TTG ATT Asp Ser Glu Lys Met Val Ala Asp Leu Glu Asn Pro Tyr Ile Leu Ile 205 210 215 220	674
ACA GAC AAG AAA ATT TCC AAT ATC CAA GAA ATC TTG CCA CTT TTG GAA Thr Asp Lys Lys Ile Ser Asn Ile Gln Glu Ile Leu Pro Leu Leu Glu 225 230 235	722
AGC ATT CTC CAA AGC AAT CGT CCA CTC TTG ATT ATT GCG GAT GAT GTG Ser Ile Leu Gln Ser Asn Arg Pro Leu Leu Ile Ile Ala Asp Asp Val 240 245 250	770
GAT GGT GAG GCT CTT CCA ACT CTT GTT TTG AAC AAG ATT CGT GGA ACC Asp Gly Glu Ala Leu Pro Thr Leu Val Leu Asn Lys Ile Arg Gly Thr 255 260 265	818
TTC AAC GTA GTA GCA GTC AAG GCA CCT GGT TTT GGT GAC CGT CGC AAA Phe Asn Val Val Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys 270 275 280	866
GCC ATG CTT GAA GAT ATC GCC ATC TTA ACA GGC GGA ACA GTT ATC ACA	914



Ala Met Leu Glu Asp Ile Ala Ile Leu Thr Gly Gly Thr Val Ile Thr 285 290 295 300	
GAA GAC CTT GGT CTT GAG TTG AAA GAT GCG ACA ATT GAA GCT CTT GGT Glu Asp Leu Gly Leu Glu Leu Lys Asp Ala Thr Ile Glu Ala Leu Gly 305 310 315	962
CAA GCA GCG AGA GTG ACC GTG GAC AAA GAT AGC ACG GTT ATT GTA GAA Gln Ala Ala Arg Val Thr Val Asp Lys Asp Ser Thr Val Ile Val Glu 320 325 330	1010
GGT GCA GGA AAT CCT GAA GCG ATT TCT CAC CGT GTT GCG GTT ATC AAG Gly Ala Gly Asn Pro Glu Ala Ile Ser His Arg Val Ala Val Ile Lys 335 340 345	1058
TCT CAA ATC GAA ACT ACA ACT TCT GAA TTT GAC CGT GAA AAA TTG CAA Ser Gln Ile Glu Thr Thr Thr Ser Glu Phe Asp Arg Glu Lys Leu Gln 350 355 360	1106
GAA CGC TTG GCC AAA TTG TCA GGT GGT GTA GCG GTT ATT AAG GTC GGA Glu Arg Leu Ala Lys Leu Ser Gly Gly Val Ala Val Ile Lys Val Gly 365 370 375 380	1154
GCC GCA ACT GAA ACT GAG TTG AAA GAA ATG AAA CTC CGC ATT GAA GAT Ala Ala Thr Glu Thr Glu Leu Lys Glu Met Lys Leu Arg Ile Glu Asp 385 390 395	1202
GCC CTC AAC GCT ACT CGT GCA GCT GTT GAA GAA GGT ATT GTT GCA GGT Ala Leu Asn Ala Thr Arg Ala Ala Val Glu Glu Gly Ile Val Ala Gly 400 405 410	1250
GGT GGA ACA GCT CTT GCC AAT GTG ATT CCA GCT GTT GCT ACC TTG GAA Gly Gly Thr Ala Leu Ala Asn Val Ile Pro Ala Val Ala Thr Leu Glu 415 420 425	1298
TTG ACA GGA GAT GAA GCA ACA GGA CGT AAT ATT GTT CTC CGT GCT TTG Leu Thr Gly Asp Glu Ala Thr Gly Arg Asn Ile Val Leu Arg Ala Leu 430 435 440	1346
GAA GAA CCT GTT CGT CAA ATT GCT CAC AAT GCA GGA TTT GAA GGA TCT Glu Glu Pro Val Arg Gln Ile Ala His Asn Ala Gly Phe Glu Gly Ser 445 450 455 460	1394
ATC GTT ATC GAT CGT TTG AAA AAT GCT GAG CTT GGT ATA GGA TTC AAC Ile Val Ile Asp Arg Leu Lys Asn Ala Glu Leu Gly Ile Gly Phe Asn 465 470 475	1442
GCA GCA ACT GGC GAG TGG GTT AAC ATG ATT GAT CAA GGT ATC ATT GAT Ala Ala Thr Gly Glu Trp Val Asn Met Ile Asp Gln Gly Ile Ile Asp 480 485 490	1490
CCA GTT AAA GTG AGT CGT TCA GCC CTA CAA AAT GCA GCA TCT GTA GCC Pro Val Lys Val Ser Arg Ser Ala Leu Gln Asn Ala Ala Ser Val Ala 495 500 505	1538
AGC TTG ATT TTG ACA ACA GAA GCA GTC GTA GCC AAT AAA CCA GAA CCA Ser Leu Ile Leu Thr Thr Glu Ala Val Val Ala Asn Lys Pro Glu Pro 510 515 520	1586



195					200					205					
Met	Val	Ala	Asp	Leu	Glu	Asn	Pro	Tyr	Ile	Leu	Ile	Thr	Asp	Lys	Lys
	210					215					220				
Ile	Ser	Asn	Ile	Gln	Glu	Ile	Leu	Pro	Leu	Leu	Glu	Ser	Ile	Leu	Gln
225				230						235					240
Ser	Asn	Arg	Pro	Leu	Leu	Ile	Ile	Ala	Asp	Asp	Val	Asp	Gly	Glu	Ala
			245						250					255	
Leu	Pro	Thr	Leu	Val	Leu	Asn	Lys	Ile	Arg	Gly	Thr	Phe	Asn	Val	Val
		260						265					270		
Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Met	Leu	Glu
	275						280					285			
Asp	Ile	Ala	Ile	Leu	Thr	Gly	Gly	Thr	Val	Ile	Thr	Glu	Asp	Leu	Gly
290						295					300				
Leu	Glu	Leu	Lys	Asp	Ala	Thr	Ile	Glu	Ala	Leu	Gly	Gln	Ala	Ala	Arg
305				310						315					320
Val	Thr	Val	Asp	Lys	Asp	Ser	Thr	Val	Ile	Val	Glu	Gly	Ala	Gly	Asn
			325						330					335	
Pro	Glu	Ala	Ile	Ser	His	Arg	Val	Ala	Val	Ile	Lys	Ser	Gln	Ile	Glu
		340						345					350		
Thr	Thr	Thr	Ser	Glu	Phe	Asp	Arg	Glu	Lys	Leu	Gln	Glu	Arg	Leu	Ala
		355					360					365			
Lys	Leu	Ser	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	Ala	Ala	Thr	Glu
370						375					380				
Thr	Glu	Leu	Lys	Glu	Met	Lys	Leu	Arg	Ile	Glu	Asp	Ala	Leu	Asn	Ala
385				390						395					400
Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Ala	Gly	Gly	Gly	Thr	Ala
			405						410					415	
Leu	Ala	Asn	Val	Ile	Pro	Ala	Val	Ala	Thr	Leu	Glu	Leu	Thr	Gly	Asp
		420						425					430		
Glu	Ala	Thr	Gly	Arg	Asn	Ile	Val	Leu	Arg	Ala	Leu	Glu	Glu	Pro	Val
	435						440					445			
Arg	Gln	Ile	Ala	His	Asn	Ala	Gly	Phe	Glu	Gly	Ser	Ile	Val	Ile	Asp
450					455						460				
Arg	Leu	Lys	Asn	Ala	Glu	Leu	Gly	Ile	Gly	Phe	Asn	Ala	Ala	Thr	Gly
465				470						475					480
Glu	Trp	Val	Asn	Met	Ile	Asp	Gln	Gly	Ile	Ile	Asp	Pro	Val	Lys	Val
			485						490					495	
Ser	Arg	Ser	Ala	Leu	Gln	Asn	Ala	Ala	Ser	Val	Ala	Ser	Leu	Ile	Leu
		500						505					510		

Thr Thr Glu Ala Val Val Ala Asn Lys Pro Glu Pro Val Ala Pro Ala  
515 520 525

Pro Ala Met Asp Pro Ser Met Met Gly Gly Met Gly Gly  
530 535 540

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 15..1646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGGCT TCAT ATG GCG GCT AAA GAT GTA AAA TTC GGT AAC GAC GCT	50
Met Ala Ala Lys Asp Val Lys Phe Gly Asn Asp Ala	
1 5 10	
CGT GTA AAA ATG CTC CGC GGC GTA AAC GTA CTG GCA GAC GCA GTT AAA	98
Arg Val Lys Met Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys	
15 20 25	
GTA ACC CTG GGC CCG AAA GGC CGT AAC GTA GTG CTG GAC AAA TCC TTC	146
Val Thr Leu Gly Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe	
30 35 40	
GGC GCG CCA ACC ATC ACG AAA GAT GGT GTT TCT GTA GCA CGT GAA ATC	194
Gly Ala Pro Thr Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile	
45 50 55 60	
GAG CTG GAA GAC AAG TTC GAA AAC ATG GGC GCG CAG ATG GTG AAA GAA	242
Glu Leu Glu Asp Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu	
65 70 75	
GTG GCC TCT AAA GCG AAC GAC GCT GCA GGC GAC GGT ACC ACC ACC GCG	290
Val Ala Ser Lys Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala	
80 85 90	
ACC GTG CTG GCT CAG GCT ATC ATC ACC GAA GGT CTG AAA GCC GTT GCT	338
Thr Val Leu Ala Gln Ala Ile Ile Thr Glu Gly Leu Lys Ala Val Ala	
95 100 105	
GCG GGC ATG AAC CCA ATG GAT CTG AAA CGT GGT ATC GAC AAA GCT GTC	386
Ala Gly Met Asn Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val	
110 115 120	
GCG TCC GCT GTT GAA GAA CTG AAA GCG CTG TCC GTA CCG TGC TCT GAC	434
Ala Ser Ala Val Glu Glu Leu Lys Ala Leu Ser Val Pro Cys Ser Asp	

125		130		135		140	
TCT AAA GCC ATT GCT CAG GTA GGT ACC ATC TCC GCT AAC TCC GAC GAA	482						
Ser Lys Ala Ile Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu							
		145		150		155	
ACC GTA GGT AAA CTG ATC GCG GAA GCG ATG GAT AAA GTC GGT AAA GAA	530						
Thr Val Gly Lys Leu Ile Ala Glu Ala Met Asp Lys Val Gly Lys Glu							
		160		165		170	
GGC GTG ATC ACC GTT GAA GAC GGT ACC GGT CTG GAA GAC GAA CTG GAC	578						
Gly Val Ile Thr Val Glu Asp Gly Thr Gly Leu Glu Asp Glu Leu Asp							
		175		180		185	
GTG GTT GAA GGT ATG CAG TTC GAC CGC GGT TAC CTG TCC CCA TAC TTC	626						
Val Val Glu Gly Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe							
		190		195		200	
ATC AAC AAG CCA GAA ACT GGC GCT GTT GAG CTG GAA AGC CCG TTC ATC	674						
Ile Asn Lys Pro Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile							
		205		210		215	
CTG CTG GCT GAC AAG AAA ATC TCC AAC ATC CGC GAA ATG CTG CCA GTG	722						
Leu Leu Ala Asp Lys Lys Ile Ser Asn Ile Arg Glu Met Leu Pro Val							
		225		230		235	
CTG GAA GCC GTT GCG AAA GCA GGC AAA CCG CTG GTT ATC ATT GCT GAA	770						
Leu Glu Ala Val Ala Lys Ala Gly Lys Pro Leu Val Ile Ile Ala Glu							
		240		245		250	
GAC GTT GAA GGC GAA GCG CTG GCG ACC CTG GTG GTT AAC ACC ATG CGT	818						
Asp Val Glu Gly Glu Ala Leu Ala Thr Leu Val Val Asn Thr Met Arg							
		255		260		265	
GGC ATC GTG AAA GTG GCT GCG GTT AAA GCA CCT GGC TTC GGC GAC CGC	866						
Gly Ile Val Lys Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg							
		270		275		280	
CGT AAA GCG ATG CTG CAG GAT ATC GCT ACC CTG ACC GGC GGT ACC GTC	914						
Arg Lys Ala Met Leu Gln Asp Ile Ala Thr Leu Thr Gly Gly Thr Val							
		285		290		295	
ATC TCT GAA GAG ATC GGT ATG GAG CTG GAA AAA GCG ACC CTG GAA GAC	962						
Ile Ser Glu Glu Ile Gly Met Glu Leu Glu Lys Ala Thr Leu Glu Asp							
		305		310		315	
CTG GGC CAG GCT AAA CGT GTT GTG ATC AAC AAA GAC ACC ACC ACC ATC	1010						
Leu Gly Gln Ala Lys Arg Val Val Ile Asn Lys Asp Thr Thr Thr Ile							
		320		325		330	
ATC GAT GGC GTG GGC GAC GAA GCG GCG ATT CAG GGC CGT GTT GGT CAG	1058						
Ile Asp Gly Val Gly Asp Glu Ala Ala Ile Gln Gly Arg Val Gly Gln							
		335		340		345	
ATC CGT AAG CAG ATC GAA GAA GCC ACT TCC GAT TAC GAC CGT GAA AAA	1106						
Ile Arg Lys Gln Ile Glu Glu Ala Thr Ser Asp Tyr Asp Arg Glu Lys							
		350		355		360	

CTG CAG GAG CGC GTA GCG AAA CTG GCA GGC GGT GTT GCG GTA ATC AAA Leu Gln Glu Arg Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys 365 370 375 380	1154
GTC GGT GCT GCG ACT GAA GTT GAA ATG AAA GAG AAA AAA GCA CGC GTT Val Gly Ala Ala Thr Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val 385 390 395	1202
GAC GAT GCC CTG CAC GCG ACC CGT GCT GCG GTA GAA GAA GGC GTG GTT Asp Asp Ala Leu His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val 400 405 410	1250
GCT GGT GGT GGT GTG GCG CTG GTG CGT GTT GCC GCG AAA CTG TCC GGC Ala Gly Gly Gly Val Ala Leu Val Arg Val Ala Ala Lys Leu Ser Gly 415 420 425	1298
CTG ACT GCT CAG AAC GAA GAT CAG AAC GTG GGT ATC AAA GTT GCG CTG Leu Thr Ala Gln Asn Glu Asp Gln Asn Val Gly Ile Lys Val Ala Leu 430 435 440	1346
CGC GCA ATG GAA GCT CCA CTG CGT CAG ATC GTG TCC AAC GCC GGT GAA Arg Ala Met Glu Ala Pro Leu Arg Gln Ile Val Ser Asn Ala Gly Glu 445 450 455 460	1394
GAG CCA TCT GTT GTG ACC AAC AAC GTG AAA GCA GGC GAA GGT AAC TAC Glu Pro Ser Val Val Thr Asn Asn Val Lys Ala Gly Glu Gly Asn Tyr 465 470 475	1442
GGT TAC AAC GCA GCA ACT GAA GAA TAC GGC AAC ATG ATC GAC TTC GGT Gly Tyr Asn Ala Ala Thr Glu Glu Tyr Gly Asn Met Ile Asp Phe Gly 480 485 490	1490
ATC CTG GAT CCA ACC AAA GTG ACC CGT TCT GCT CTG CAG TAC GCG GCA Ile Leu Asp Pro Thr Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala 495 500 505	1538
TCT GTC GCT GGC CTG ATG ATC ACC ACC GAG TGC ATG GTG ACC GAC CTG Ser Val Ala Gly Leu Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu 510 515 520	1586
CCT AAA GGC GAC GCA CCT GAC TTA GGT GCT GCA GGC ATG GGT GGG ATG Pro Lys Gly Asp Ala Pro Asp Leu Gly Ala Ala Gly Met Gly Gly Met 525 530 535 540	1634
GGC GGT ATG ATG TGATCAAGCC GAATTC Gly Gly Met Met	1662

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ala	Ala	Lys	Asp	Val	Lys	Phe	Gly	Asn	Asp	Ala	Arg	Val	Lys	Met	
1				5					10					15		
Leu	Arg	Gly	Val	Asn	Val	Leu	Ala	Asp	Ala	Val	Lys	Val	Thr	Leu	Gly	
			20					25					30			
Pro	Lys	Gly	Arg	Asn	Val	Val	Leu	Asp	Lys	Ser	Phe	Gly	Ala	Pro	Thr	
		35					40					45				
Ile	Thr	Lys	Asp	Gly	Val	Ser	Val	Ala	Arg	Glu	Ile	Glu	Leu	Glu	Asp	
	50					55					60					
Lys	Phe	Glu	Asn	Met	Gly	Ala	Gln	Met	Val	Lys	Glu	Val	Ala	Ser	Lys	
65					70					75					80	
Ala	Asn	Asp	Ala	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	
				85					90					95		
Gln	Ala	Ile	Ile	Thr	Glu	Gly	Leu	Lys	Ala	Val	Ala	Ala	Gly	Met	Asn	
			100					105					110			
Pro	Met	Asp	Leu	Lys	Arg	Gly	Ile	Asp	Lys	Ala	Val	Ala	Ser	Ala	Val	
		115					120					125				
Glu	Glu	Leu	Lys	Ala	Leu	Ser	Val	Pro	Cys	Ser	Asp	Ser	Lys	Ala	Ile	
	130					135					140					
Ala	Gln	Val	Gly	Thr	Ile	Ser	Ala	Asn	Ser	Asp	Glu	Thr	Val	Gly	Lys	
145					150					155					160	
Leu	Ile	Ala	Glu	Ala	Met	Asp	Lys	Val	Gly	Lys	Glu	Gly	Val	Ile	Thr	
			165						170					175		
Val	Glu	Asp	Gly	Thr	Gly	Leu	Glu	Asp	Glu	Leu	Asp	Val	Val	Glu	Gly	
		180						185					190			
Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro	Tyr	Phe	Ile	Asn	Lys	Pro	
		195					200					205				
Glu	Thr	Gly	Ala	Val	Glu	Leu	Glu	Ser	Pro	Phe	Ile	Leu	Leu	Ala	Asp	
	210					215					220					
Lys	Lys	Ile	Ser	Asn	Ile	Arg	Glu	Met	Leu	Pro	Val	Leu	Glu	Ala	Val	
225					230					235				240		
Ala	Lys	Ala	Gly	Lys	Pro	Leu	Val	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	
			245						250					255		
Glu	Ala	Leu	Ala	Thr	Leu	Val	Val	Asn	Thr	Met	Arg	Gly	Ile	Val	Lys	
		260						265					270			
Val	Ala	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Met	
		275					280					285				
Leu	Gln	Asp	Ile	Ala	Thr	Leu	Thr	Gly	Gly	Thr	Val	Ile	Ser	Glu	Glu	
	290					295					300					

Ile	Gly	Met	Glu	Leu	Glu	Lys	Ala	Thr	Leu	Glu	Asp	Leu	Gly	Gln	Ala	
305					310					315					320	
Lys	Arg	Val	Val	Ile	Asn	Lys	Asp	Thr	Thr	Thr	Ile	Ile	Asp	Gly	Val	
				325					330					335		
Gly	Asp	Glu	Ala	Ala	Ile	Gln	Gly	Arg	Val	Gly	Gln	Ile	Arg	Lys	Gln	
			340					345					350			
Ile	Glu	Glu	Ala	Thr	Ser	Asp	Tyr	Asp	Arg	Glu	Lys	Leu	Gln	Glu	Arg	
			355				360					365				
Val	Ala	Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	Ala	Ala	
			370			375					380					
Thr	Glu	Val	Glu	Met	Lys	Glu	Lys	Lys	Ala	Arg	Val	Asp	Asp	Ala	Leu	
385					390					395					400	
His	Ala	Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	Val	Val	Ala	Gly	Gly	Gly	
				405					410					415		
Val	Ala	Leu	Val	Arg	Val	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Thr	Ala	Gln	
			420					425					430			
Asn	Glu	Asp	Gln	Asn	Val	Gly	Ile	Lys	Val	Ala	Leu	Arg	Ala	Met	Glu	
		435					440					445				
Ala	Pro	Leu	Arg	Gln	Ile	Val	Ser	Asn	Ala	Gly	Glu	Glu	Pro	Ser	Val	
		450				455					460					
Val	Thr	Asn	Asn	Val	Lys	Ala	Gly	Glu	Gly	Asn	Tyr	Gly	Tyr	Asn	Ala	
465					470					475					480	
Ala	Thr	Glu	Glu	Tyr	Gly	Asn	Met	Ile	Asp	Phe	Gly	Ile	Leu	Asp	Pro	
				485					490					495		
Thr	Lys	Val	Thr	Arg	Ser	Ala	Leu	Gln	Tyr	Ala	Ala	Ser	Val	Ala	Gly	
			500					505					510			
Leu	Met	Ile	Thr	Thr	Glu	Cys	Met	Val	Thr	Asp	Leu	Pro	Lys	Gly	Asp	
		515					520					525				
Ala	Pro	Asp	Leu	Gly	Ala	Ala	Gly	Met	Gly	Gly	Met	Gly	Gly	Met	Met	
		530				535					540					

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS



(B) LOCATION: 15..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTCGGCT TCAT ATG GCA AAA GAA ATC AAA TTT TCA GCA GAT GCG CGT	50
Met Ala Lys Glu Ile Lys Phe Ser Ala Asp Ala Arg	
1 5 10	
GCT GCC ATG GTG CGC GGA GTT GAT ATG TTA GCA GAT ACC GTC AAA GTA	98
Ala Ala Met Val Arg Gly Val Asp Met Leu Ala Asp Thr Val Lys Val	
15 20 25	
ACG CTT GGT CCT AAA GGG CGC AAT GTT GTT CTT GAA AAA GCT TTT GGT	146
Thr Leu Gly Pro Lys Gly Arg Asn Val Val Leu Glu Lys Ala Phe Gly	
30 35 40	
TCT CCC TTA ATT ACT AAT GAC GGG GTA ACC ATT GCT AAA GAG ATC GAA	194
Ser Pro Leu Ile Thr Asn Asp Gly Val Thr Ile Ala Lys Glu Ile Glu	
45 50 55 60	
TTA GAA GAT CAT TTT GAA AAC ATG GGA GCA AAA TTG GTG TCT GAA GTG	242
Leu Glu Asp His Phe Glu Asn Met Gly Ala Lys Leu Val Ser Glu Val	
65 70 75	
GCT TCT AAA ACC AAT GAT ATT GCT GGT GAT GGG ACG ACT ACT GCA ACA	290
Ala Ser Lys Thr Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr	
80 85 90	
GTT TTG ACA CAA GCC ATT GTT CAT GAA GGA CTA AAA AAT GTG ACA GCA	338
Val Leu Thr Gln Ala Ile Val His Glu Gly Leu Lys Asn Val Thr Ala	
95 100 105	
GGT GCT AAT CCA ATT GGT ATC CGT CGA GGC ATT GAA ACA GCA ACA GCA	386
Gly Ala Asn Pro Ile Gly Ile Arg Arg Gly Ile Glu Thr Ala Thr Ala	
110 115 120	
ACA GCT GTT GAA GCC TTG AAA GCC ATT GCT CAA CCT GTA TCT GGC AAG	434
Thr Ala Val Glu Ala Leu Lys Ala Ile Ala Gln Pro Val Ser Gly Lys	
125 130 135 140	
GAA GCT ATT GCT CAG GTC GCT GCA GTA TCA TCA CGC TCT GAA AAA GTT	482
Glu Ala Ile Ala Gln Val Ala Ala Val Ser Ser Arg Ser Glu Lys Val	
145 150 155	
GGA GAG TAT ATC TCA GAA GCT ATG GAG CGT GTG GGC AAC GAT GGT GTG	530
Gly Glu Tyr Ile Ser Glu Ala Met Glu Arg Val Gly Asn Asp Gly Val	
160 165 170	
ATT ACC ATC GAA GAA TCT CGA GGT ATG GAA ACA GAA CTT GAA GTG GTT	578
Ile Thr Ile Glu Glu Ser Arg Gly Met Glu Thr Glu Leu Glu Val Val	
175 180 185	
GAA GGC ATG CAA TTT GAC CGT GGT TAC CTG TCT CAA TAC ATG GTC ACA	626
Glu Gly Met Gln Phe Asp Arg Gly Tyr Leu Ser Gln Tyr Met Val Thr	
190 195 200	
GAC AAT GAA AAA ATG GTT GCA GAC CTT GAA AAC CCA TTT ATC TTA ATC	674

Asp	Asn	Glu	Lys	Met	Val	Ala	Asp	Leu	Glu	Asn	Pro	Phe	Ile	Leu	Ile	
205					210					215					220	
ACG	GAT	AAA	AAA	GTG	TCA	AAC	ATC	CAA	GAC	ATT	TTG	CCA	CTA	CTT	GAG	722
Thr	Asp	Lys	Lys	Val	Ser	Asn	Ile	Gln	Asp	Ile	Leu	Pro	Leu	Leu	Glu	
				225					230						235	
GAA	GTT	CTT	AAA	ACC	AAC	CGT	CCA	TTA	CTC	ATT	ATT	GCA	GAT	GAT	GTG	770
Glu	Val	Leu	Lys	Thr	Asn	Arg	Pro	Leu	Leu	Ile	Ile	Ala	Asp	Asp	Val	
			240					245					250			
GAT	GGT	GAA	GCA	CTT	CCA	ACC	CTT	GTC	TTG	AAC	AAG	ATT	CGT	GGT	ACT	818
Asp	Gly	Glu	Ala	Leu	Pro	Thr	Leu	Val	Leu	Asn	Lys	Ile	Arg	Gly	Thr	
		255					260					265				
TTC	AAT	GTG	GTT	GCT	GTC	AAA	GCG	CCA	GGA	TTT	GGT	GAT	CGT	CGT	AAA	866
Phe	Asn	Val	Val	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	
	270					275					280					
GCT	ATG	CTT	GAA	GAC	ATT	GCT	ATC	TTG	ACA	GGT	GGT	ACA	GTG	ATT	ACA	914
Ala	Met	Leu	Glu	Asp	Ile	Ala	Ile	Leu	Thr	Gly	Gly	Thr	Val	Ile	Thr	
285					290					295					300	
GAG	GAT	CTA	GGA	CTT	GAA	TTA	AAA	GAT	GCT	ACA	ATG	ACA	GCC	CTT	GGA	962
Glu	Asp	Leu	Gly	Leu	Glu	Leu	Lys	Asp	Ala	Thr	Met	Thr	Ala	Leu	Gly	
				305					310					315		
CAG	GCT	GCT	AAG	ATT	ACA	GTT	GAT	AAA	GAT	AGC	ACA	GTA	ATT	GTT	GAA	1010
Gln	Ala	Ala	Lys	Ile	Thr	Val	Asp	Lys	Asp	Ser	Thr	Val	Ile	Val	Glu	
			320					325					330			
GGT	TCA	GGA	AGT	TCA	GAA	GCT	ATT	GCT	AAC	CGT	ATT	GCA	CTG	ATT	AAA	1058
Gly	Ser	Gly	Ser	Ser	Glu	Ala	Ile	Ala	Asn	Arg	Ile	Ala	Leu	Ile	Lys	
		335					340					345				
TCG	CAA	TTA	GAA	ACA	ACA	ACT	TCT	GAC	TTT	GAC	CGT	GAA	AAA	CTA	CAA	1106
Ser	Gln	Leu	Glu	Thr	Thr	Thr	Ser	Asp	Phe	Asp	Arg	Glu	Lys	Leu	Gln	
	350					355					360					
GAA	CGT	TTG	GCG	AAA	TTA	GCT	GGT	GGT	GTA	GCT	GTT	ATC	AAA	GTA	GGA	1154
Glu	Arg	Leu	Ala	Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	
365					370					375					380	
GCT	CCA	ACA	GAG	ACA	GCT	TTA	AAA	GAA	ATG	AAA	CTT	CGC	ATT	GAG	GAT	1202
Ala	Pro	Thr	Glu	Thr	Ala	Leu	Lys	Glu	Met	Lys	Leu	Arg	Ile	Glu	Asp	
				385					390					395		
GCT	CTA	AAT	GCT	ACA	CGT	GCA	GCC	GTT	GAA	GAA	GGT	ATC	GTT	GCT	GGT	1250
Ala	Leu	Asn	Ala	Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Ala	Gly	
			400					405					410			
GGT	GGA	ACA	GCA	CTT	ATT	ACG	GTT	ATT	GAA	AAA	GTA	GCA	GCT	CTT	GAG	1298
Gly	Gly	Thr	Ala	Leu	Ile	Thr	Val	Ile	Glu	Lys	Val	Ala	Ala	Leu	Glu	
		415					420					425				
CTT	GAG	GGC	GAT	GAT	GCT	ACT	GGA	CGT	AAC	ATT	GTG	CTT	CGT	GCT	CTA	1346
Leu	Glu	Gly	Asp	Asp	Ala	Thr	Gly	Arg	Asn	Ile	Val	Leu	Arg	Ala	Leu	
	430					435					440					

GAA GAG CCT GTA CGT CAA ATT GCT TTA AAT GCT GGG TAC GAA GGC TCC	1394
Glu Glu Pro Val Arg Gln Ile Ala Leu Asn Ala Gly Tyr Glu Gly Ser	
445 450 455 460	
GTA GTT ATT GAC AAG TTG AAA AAC AGC CCT GCA GGA ACA GGA TTT AAT	1442
Val Val Ile Asp Lys Leu Lys Asn Ser Pro Ala Gly Thr Gly Phe Asn	
465 470 475	
GCT GCA ACA GGT GAG TGG GTT GAT ATG ATT AAA ACA GGA ATC ATT GAC	1490
Ala Ala Thr Gly Glu Trp Val Asp Met Ile Lys Thr Gly Ile Ile Asp	
480 485 490	
CCT GTC AAA GTA ACA CGA TCA GCG CTT CAA AAT GCA GCT TCT GTA GCT	1538
Pro Val Lys Val Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Val Ala	
495 500 505	
AGT CTT ATT TTG ACA ACA GAA GCA GTT GTT GCT AAT AAA CCT GAA CCA	1586
Ser Leu Ile Leu Thr Thr Glu Ala Val Val Ala Asn Lys Pro Glu Pro	
510 515 520	
GCT ACG CCA GCG CCA GCA ATG CCA GCA GGT ATG GAT CCA GGA ATG ATG	1634
Ala Thr Pro Ala Pro Ala Met Pro Ala Gly Met Asp Pro Gly Met Met	
525 530 535 540	
GGT GGG ATG GGC GGA TAAGCCGAAT TC	1661
Gly Gly Met Gly Gly	
545	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Lys Glu Ile Lys Phe Ser Ala Asp Ala Arg Ala Ala Met Val	
1 5 10 15	
Arg Gly Val Asp Met Leu Ala Asp Thr Val Lys Val Thr Leu Gly Pro	
20 25 30	
Lys Gly Arg Asn Val Val Leu Glu Lys Ala Phe Gly Ser Pro Leu Ile	
35 40 45	
Thr Asn Asp Gly Val Thr Ile Ala Lys Glu Ile Glu Leu Glu Asp His	
50 55 60	
Phe Glu Asn Met Gly Ala Lys Leu Val Ser Glu Val Ala Ser Lys Thr	
65 70 75 80	
Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Thr Gln	
85 90 95	

Ala	Ile	Val	His	Glu	Gly	Leu	Lys	Asn	Val	Thr	Ala	Gly	Ala	Asn	Pro	100	105	110
Ile	Gly	Ile	Arg	Arg	Gly	Ile	Glu	Thr	Ala	Thr	Ala	Thr	Ala	Val	Glu	115	120	125
Ala	Leu	Lys	Ala	Ile	Ala	Gln	Pro	Val	Ser	Gly	Lys	Glu	Ala	Ile	Ala	130	135	140
Gln	Val	Ala	Ala	Val	Ser	Ser	Arg	Ser	Glu	Lys	Val	Gly	Glu	Tyr	Ile	145	150	155
Ser	Glu	Ala	Met	Glu	Arg	Val	Gly	Asn	Asp	Gly	Val	Ile	Thr	Ile	Glu	165	170	175
Glu	Ser	Arg	Gly	Met	Glu	Thr	Glu	Leu	Glu	Val	Val	Glu	Gly	Met	Gln	180	185	190
Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Gln	Tyr	Met	Val	Thr	Asp	Asn	Glu	Lys	195	200	205
Met	Val	Ala	Asp	Leu	Glu	Asn	Pro	Phe	Ile	Leu	Ile	Thr	Asp	Lys	Lys	210	215	220
Val	Ser	Asn	Ile	Gln	Asp	Ile	Leu	Pro	Leu	Leu	Glu	Glu	Val	Leu	Lys	225	230	235
Thr	Asn	Arg	Pro	Leu	Leu	Ile	Ile	Ala	Asp	Asp	Val	Asp	Gly	Glu	Ala	245	250	255
Leu	Pro	Thr	Leu	Val	Leu	Asn	Lys	Ile	Arg	Gly	Thr	Phe	Asn	Val	Val	260	265	270
Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Met	Leu	Glu	275	280	285
Asp	Ile	Ala	Ile	Leu	Thr	Gly	Gly	Thr	Val	Ile	Thr	Glu	Asp	Leu	Gly	290	295	300
Leu	Glu	Leu	Lys	Asp	Ala	Thr	Met	Thr	Ala	Leu	Gly	Gln	Ala	Ala	Lys	305	310	315
Ile	Thr	Val	Asp	Lys	Asp	Ser	Thr	Val	Ile	Val	Glu	Gly	Ser	Gly	Ser	325	330	335
Ser	Glu	Ala	Ile	Ala	Asn	Arg	Ile	Ala	Leu	Ile	Lys	Ser	Gln	Leu	Glu	340	345	350
Thr	Thr	Thr	Ser	Asp	Phe	Asp	Arg	Glu	Lys	Leu	Gln	Glu	Arg	Leu	Ala	355	360	365
Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	Ala	Pro	Thr	Glu	370	375	380
Thr	Ala	Leu	Lys	Glu	Met	Lys	Leu	Arg	Ile	Glu	Asp	Ala	Leu	Asn	Ala	385	390	395

Thr Arg Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Gly Thr Ala  
 405 410 415  
 Leu Ile Thr Val Ile Glu Lys Val Ala Ala Leu Glu Leu Glu Gly Asp  
 420 425 430  
 Asp Ala Thr Gly Arg Asn Ile Val Leu Arg Ala Leu Glu Glu Pro Val  
 435 440 445  
 Arg Gln Ile Ala Leu Asn Ala Gly Tyr Glu Gly Ser Val Val Ile Asp  
 450 455 460  
 Lys Leu Lys Asn Ser Pro Ala Gly Thr Gly Phe Asn Ala Ala Thr Gly  
 465 470 475 480  
 Glu Trp Val Asp Met Ile Lys Thr Gly Ile Ile Asp Pro Val Lys Val  
 485 490 495  
 Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Val Ala Ser Leu Ile Leu  
 500 505 510  
 Thr Thr Glu Ala Val Val Ala Asn Lys Pro Glu Pro Ala Thr Pro Ala  
 515 520 525  
 Pro Ala Met Pro Ala Gly Met Asp Pro Gly Met Met Gly Gly Met Gly  
 530 535 540  
 Gly  
 545

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Lys Glu Ile Lys Phe Ser Glu Glu Ala Arg Arg Ala Met Leu  
 1 5 10 15  
 Arg Gly Val Asp Ala Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro  
 20 25 30  
 Lys Gly Arg Asn Val Val Leu Glu Lys Lys Phe Gly Ser Pro Leu Ile  
 35 40 45  
 Thr Asn Asp Gly Val Thr Ile Ala Lys Glu Ile Glu Leu Glu Asp Ala  
 50 55 60  
 Phe Glu Asn Met Gly Ala Lys Leu Val Ala Glu Val Ala Ser Lys Thr  
 65 70 75 80

Asn	Asp	Val	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	Gln	
				85					90					95		
Ala	Met	Ile	Arg	Glu	Gly	Leu	Lys	Asn	Val	Thr	Ala	Gly	Ala	Asn	Pro	
				100					105					110		
Val	Gly	Val	Arg	Lys	Gly	Met	Glu	Gln	Ala	Val	Ala	Val	Ala	Ile	Glu	
				115					120					125		
Asn	Leu	Lys	Glu	Ile	Ser	Lys	Pro	Ile	Glu	Gly	Lys	Glu	Ser	Ile	Ala	
				130					135					140		
Gln	Val	Ala	Ala	Ile	Ser	Ala	Ala	Asp	Glu	Glu	Val	Gly	Ser	Leu	Ile	
				145					150					155		
Ala	Glu	Ala	Met	Glu	Arg	Val	Gly	Asn	Asp	Gly	Val	Ile	Thr	Ile	Glu	
				165					170					175		
Glu	Ser	Lys	Gly	Phe	Thr	Thr	Glu	Leu	Glu	Val	Val	Glu	Gly	Met	Gln	
				180					185					190		
Phe	Asp	Arg	Gly	Tyr	Ala	Ser	Pro	Tyr	Met	Val	Thr	Asp	Ser	Asp	Lys	
				195					200					205		
Met	Glu	Ala	Val	Leu	Asp	Asn	Pro	Tyr	Ile	Leu	Ile	Thr	Asp	Lys	Lys	
				210					215					220		
Ile	Thr	Asn	Ile	Gln	Glu	Ile	Leu	Pro	Val	Leu	Glu	Gln	Val	Val	Gln	
				225					230					235		
Gln	Gly	Lys	Pro	Leu	Leu	Leu	Ile	Ala	Glu	Asp	Val	Glu	Gly	Glu	Ala	
				245					250					255		
Leu	Ala	Thr	Leu	Val	Val	Asn	Lys	Leu	Arg	Gly	Thr	Phe	Asn	Ala	Val	
				260					265					270		
Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Met	Leu	Glu	
				275					280					285		
Asp	Ile	Ala	Val	Leu	Thr	Gly	Gly	Glu	Val	Ile	Thr	Glu	Asp	Leu	Gly	
				290					295					300		
Leu	Asp	Leu	Lys	Ser	Thr	Gln	Ile	Ala	Gln	Leu	Gly	Arg	Ala	Ser	Lys	
				305					310					315		
Val	Val	Val	Thr	Lys	Glu	Asn	Thr	Thr	Ile	Val	Glu	Gly	Ala	Gly	Glu	
				325					330					335		
Thr	Asp	Lys	Ile	Ser	Ala	Arg	Val	Thr	Gln	Ile	Arg	Ala	Gln	Val	Glu	
				340					345					350		
Glu	Thr	Thr	Ser	Glu	Phe	Asp	Arg	Glu	Lys	Leu	Gln	Glu	Arg	Leu	Ala	
				355					360					365		
Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	Ala	Ala	Thr	Glu	
				370					375					380		

Thr	Glu	Leu	Lys	Glu	Arg	Lys	Leu	Arg	Ile	Glu	Asp	Ala	Leu	Asn	Ser	385	390	395	400
Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Ser	Gly	Gly	Gly	Thr	Ala	405	410	415	
Leu	Val	Asn	Val	Tyr	Asn	Lys	Val	Ala	Ala	Val	Glu	Ala	Glu	Gly	Asp	420	425	430	
Ala	Gln	Thr	Gly	Ile	Asn	Ile	Val	Leu	Arg	Ala	Leu	Glu	Glu	Pro	Ile	435	440	445	
Arg	Gln	Ile	Ala	His	Asn	Ala	Gly	Leu	Glu	Gly	Ser	Val	Ile	Val	Glu	450	455	460	
Arg	Leu	Lys	Asn	Glu	Glu	Ile	Gly	Val	Gly	Phe	Asn	Ala	Ala	Thr	Gly	465	470	475	480
Glu	Trp	Val	Asn	Met	Ile	Glu	Lys	Gly	Ile	Val	Asp	Pro	Thr	Lys	Val	485	490	495	
Thr	Arg	Ser	Ala	Leu	Gln	Asn	Ala	Ala	Ser	Val	Ala	Ala	Met	Phe	Leu	500	505	510	
Thr	Thr	Glu	Ala	Val	Val	Ala	Asp	Lys	Pro	Glu	Glu	Asn	Gly	Gly	Gly	515	520	525	
Ala	Gly	Met	Pro	Asp	Met	Gly	Gly	Met	Gly	Gly	Met	Gly	Gly	Met	Met	530	535	540	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ala	Lys	Thr	Leu	Leu	Phe	Gly	Glu	Glu	Ala	Arg	Arg	Ser	Met	Gln	1	5	10	15
Ala	Gly	Val	Asp	Lys	Leu	Ala	Asn	Thr	Val	Lys	Val	Thr	Leu	Gly	Pro	20	25	30	
Lys	Gly	Arg	Asn	Val	Ile	Leu	Asp	Lys	Lys	Phe	Gly	Ser	Pro	Leu	Ile	35	40	45	
Thr	Asn	Asp	Gly	Val	Thr	Ile	Ala	Arg	Glu	Ile	Glu	Leu	Glu	Asp	Ala	50	55	60	
Tyr	Glu	Asn	Met	Gly	Ala	Gln	Leu	Val	Lys	Glu	Val	Ala	Thr	Lys	Thr				

65					70					75					80
Asn	Asp	Val	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Leu	Leu	Ala	Gln
				85					90					95	
Ala	Ile	Ile	Arg	Glu	Gly	Leu	Lys	Asn	Val	Thr	Ala	Gly	Ala	Asn	Pro
			100					105					110		
Ile	Leu	Ile	Arg	Asn	Gly	Ile	Lys	Thr	Ala	Val	Glu	Lys	Ala	Val	Glu
		115					120					125			
Glu	Ile	Gln	Lys	Ile	Ser	Lys	Pro	Val	Asn	Gly	Lys	Glu	Asp	Ile	Ala
	130					135					140				
Arg	Val	Ala	Ala	Ile	Ser	Ala	Ala	Asp	Glu	Lys	Ile	Gly	Lys	Leu	Ile
145					150					155					160
Ala	Asp	Ala	Met	Glu	Lys	Val	Gly	Asn	Glu	Gly	Val	Ile	Thr	Val	Glu
				165					170					175	
Glu	Ser	Lys	Ser	Met	Gly	Thr	Glu	Leu	Asp	Val	Val	Glu	Gly	Met	Gln
			180					185					190		
Phe	Asp	Arg	Gly	Tyr	Val	Ser	Ala	Tyr	Met	Val	Thr	Asp	Thr	Glu	Lys
		195					200					205			
Met	Glu	Ala	Val	Leu	Asp	Asn	Pro	Leu	Val	Leu	Ile	Thr	Asp	Lys	Lys
	210					215					220				
Ile	Ser	Asn	Ile	Gln	Asp	Leu	Leu	Pro	Leu	Leu	Glu	Gln	Ile	Val	Gln
225					230					235					240
Ala	Gly	Lys	Lys	Leu	Leu	Ile	Ile	Ala	Asp	Asp	Ile	Glu	Gly	Glu	Ala
				245					250					255	
Met	Thr	Thr	Leu	Val	Val	Asn	Lys	Leu	Arg	Gly	Thr	Phe	Thr	Cys	Val
			260					265					270		
Gly	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Glu	Met	Leu	Gln
		275					280					285			
Asp	Ile	Ala	Thr	Leu	Thr	Gly	Gly	Val	Val	Ile	Ser	Asp	Glu	Val	Gly
	290					295					300				
Gly	Asp	Leu	Lys	Glu	Ala	Thr	Leu	Asp	Met	Leu	Gly	Glu	Ala	Glu	Ser
305					310					315				320	
Val	Lys	Val	Thr	Lys	Glu	Ser	Thr	Thr	Ile	Val	Asn	Gly	Arg	Gly	Asn
				325					330					335	
Ser	Glu	Glu	Ile	Lys	Asn	Arg	Ile	Asn	Gln	Ile	Lys	Leu	Gln	Leu	Glu
			340					345					350		
Ala	Thr	Thr	Ser	Glu	Phe	Asp	Lys	Glu	Lys	Leu	Gln	Glu	Arg	Leu	Ala
			355				360					365			
Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Val	Lys	Val	Gly	Ala	Ala	Thr	Glu
	370					375					380				



Thr	Glu	Leu	Lys	Glu	Ser	Lys	Leu	Arg	Ile	Glu	Asp	Ala	Leu	Ala	Ala	385	390	395	400
Thr	Lys	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Pro	Gly	Gly	Gly	Thr	Ala	405	410		415
Tyr	Val	Asn	Val	Ile	Asn	Glu	Val	Ala	Lys	Leu	Thr	Ser	Asp	Ile	Gln	420	425		430
Asp	Glu	Gln	Val	Gly	Ile	Asn	Ile	Ile	Val	Arg	Ser	Leu	Glu	Glu	Pro	435	440		445
Met	Arg	Gln	Ile	Ala	His	Asn	Ala	Gly	Leu	Glu	Gly	Ser	Val	Ile	Ile	450	455		460
Glu	Lys	Val	Lys	Asn	Ser	Asp	Ala	Gly	Val	Gly	Phe	Asp	Ala	Leu	Arg	465	470		475
Gly	Glu	Tyr	Lys	Asp	Met	Ile	Lys	Ala	Gly	Ile	Val	Asp	Pro	Thr	Lys	485	490		495
Val	Thr	Arg	Ser	Ala	Leu	Gln	Asn	Ala	Ala	Ser	Val	Ala	Ser	Thr	Phe	500	505		510
Leu	Thr	Thr	Glu	Ala	Ala	Val	Ala	Asp	Ile	Pro	Glu	Lys	Glu	Met	Pro	515	520		525
Gln	Gly	Ala	Gly	Met	Gly	Met	Asp	Gly	Met	Tyr						530	535		

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Ala	Asn	Met	Val	Val	Thr	Gly	Glu	Gln	Leu	Asp	Lys	Ser	Ile	Arg	1	5	10	15
Glu	Val	Val	Arg	Ile	Leu	Glu	Asp	Ala	Val	Gly	Cys	Thr	Ala	Gly	Pro	20	25	30	
Lys	Gly	Leu	Thr	Val	Ala	Ile	Ser	Lys	Pro	Tyr	Gly	Ala	Pro	Glu	Val	35	40	45	
Thr	Lys	Asp	Gly	Tyr	Lys	Val	Met	Lys	Ser	Ile	Lys	Pro	Glu	Asp	Pro	50	55	60	
Leu	Ala	Leu	Ala	Ile	Ala	Asn	Ile	Ile	Ala	Gln	Ser	Ala	Ser	Gln	Cys				

65					70						75					80
Asn	Asp	Lys	Val	Gly	Asp	Gly	Thr	Thr	Thr	Cys	Ser	Ile	Leu	Thr	Ala	
				85					90						95	
Lys	Val	Ile	Glu	Glu	Val	Ser	Lys	Val	Lys	Ala	Ala	Gly	Ala	Asp	Ile	
			100					105						110		
Ile	Cys	Val	Arg	Glu	Gly	Val	Leu	Lys	Ala	Lys	Glu	Ala	Val	Leu	Glu	
		115					120						125			
Ala	Leu	Lys	Cys	Met	Lys	Arg	Glu	Val	Leu	Ser	Glu	Glu	Glu	Ile	Ala	
		130				135						140				
Gln	Val	Ala	Thr	Ile	Ser	Ala	Asn	Gly	Asp	Lys	Asn	Ile	Gly	Thr	Lys	
145					150					155					160	
Ile	Ala	Gln	Cys	Val	Lys	Glu	Val	Gly	Lys	Asp	Gly	Val	Ile	Thr	Val	
			165						170					175		
Glu	Glu	Ser	Lys	Gly	Phe	Lys	Glu	Leu	Asp	Val	Glu	Lys	Thr	Asp	Gly	
			180					185						190		
Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro	Tyr	Phe	Val	Thr	Asn	Ser	
		195					200						205			
Glu	Lys	Met	Leu	Val	Glu	Phe	Glu	Asn	Pro	Tyr	Ile	Leu	Leu	Thr	Glu	
		210				215						220				
Lys	Lys	Leu	Asn	Ile	Ile	Gln	Pro	Leu	Leu	Pro	Ile	Leu	Glu	Asn	Ile	
225					230					235					240	
Ala	Arg	Ser	Gly	Arg	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	
				245					250					255		
Glu	Ala	Leu	Ser	Thr	Leu	Val	Leu	Asn	Lys	Leu	Arg	Gly	Gly	Leu	His	
			260					265					270			
Val	Ala	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Asp	Met	
		275					280						285			
Leu	Gly	Asp	Ile	Ala	Ile	Leu	Thr	Gly	Ala	Lys	His	Val	Ile	Asn	Asp	
		290				295						300				
Glu	Leu	Ala	Ile	Lys	Met	Glu	Asp	Leu	Thr	Leu	Cys	Asp	Leu	Gly	Thr	
305					310					315					320	
Ala	Lys	Asn	Ile	Arg	Ile	Thr	Lys	Asp	Thr	Thr	Thr	Ile	Ile	Gly	Ser	
				325					330					335		
Val	Asp	Asn	Ser	Cys	Ala	His	Val	Gln	Ser	Arg	Ile	Cys	Gln	Ile	Arg	
			340					345					350			
Met	Gln	Ile	Asp	Asn	Ser	Thr	Ser	Asp	Tyr	Asp	Lys	Glu	Lys	Leu	Gln	
		355					360					365				
Glu	Arg	Leu	Ala	Lys	Leu	Ser	Gly	Gly	Val	Ala	Val	Leu	Lys	Val	Gly	
		370				375						380				

Gly	Ser	Ser	Glu	Val	Glu	Val	Lys	Glu	Arg	Lys	Asp	Arg	Val	Glu	Asp	385	390	395	400
Ala	Leu	His	Ala	Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	Val	Val	Pro	Gly	405	410		415
Gly	Gly	Ala	Ala	Leu	Leu	Tyr	Thr	Leu	Ser	Ala	Leu	Asp	Asn	Leu	Lys	420	425		430
Ser	Lys	Asn	Asp	Asp	Glu	Gln	Leu	Gly	Ile	Asn	Ile	Val	Lys	Arg	Ala	435	440		445
Leu	Gln	Ala	Pro	Ile	Lys	Arg	Ile	Ile	Lys	Asn	Ala	Gly	Ser	Glu	Asn	450	455		460
Ala	Pro	Cys	Val	Ile	Ala	His	Leu	Leu	Lys	Gln	Asn	Asp	Lys	Glu	Leu	465	470	475	480
Ile	Phe	Asn	Val	Asp	Val	Thr	Asn	Phe	Ala	Asn	Ala	Phe	Thr	Ser	Gly	485	490		495
Val	Ile	Asp	Pro	Leu	Lys	Val	Val	Arg	Ile	Ala	Phe	Asp	Phe	Ala	Val	500	505		510
Ser	Leu	Ala	Ala	Val	Phe	Met	Thr	Leu	Asn	Ala	Ile	Val	Val	Asp	Ile	515	520		525
Pro	Ser	Lys	Asp	Asp	Asn	Ser	Ala	Ala	Gly	Gly	Ala	Gly	Met	Gly	Gly	530	535		540
Met	Gly	Gly	Met	Gly	Gly	Phe										545	550		

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Ala	Ala	Lys	Asp	Val	Lys	Phe	Gly	Asn	Asp	Ala	Arg	Val	Lys	Met	1	5	10	15
Leu	Asn	Gly	Val	Asn	Ile	Leu	Ala	Asp	Ala	Val	Lys	Val	Thr	Leu	Gly	20	25		30
Pro	Lys	Gly	Arg	Asn	Val	Val	Leu	Asp	Lys	Ser	Phe	Gly	Ala	Pro	Thr	35	40		45
Ile	Thr	Lys	Asp	Gly	Val	Ser	Val	Ala	Arg	Glu	Ile	Glu	Leu	Glu	Asp				

50						55					60					
Lys	Phe	Glu	Asn	Met	Gly	Ala	Gln	Met	Val	Lys	Glu	Val	Ala	Ser	Lys	
65					70					75					80	
Ala	Asn	Asp	Ala	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	
			85					90						95		
Gln	Ala	Ile	Val	Asn	Glu	Gly	Leu	Lys	Ala	Val	Ala	Ala	Gly	Met	Asn	
			100					105					110			
Pro	Met	Asp	Leu	Lys	Arg	Gly	Ile	Asp	Lys	Ala	Val	Asn	Ser	Val	Val	
		115					120					125				
Ala	Glu	Leu	Lys	Asn	Leu	Ser	Lys	Pro	Cys	Glu	Thr	Ser	Lys	Glu	Ile	
		130				135					140					
Glu	Gln	Val	Gly	Thr	Ile	Ser	Ala	Asn	Ser	Asp	Ser	Ile	Val	Gly	Gln	
145					150					155					160	
Leu	Ile	Ala	Gln	Ala	Met	Glu	Lys	Val	Gly	Lys	Glu	Gly	Val	Ile	Thr	
			165						170					175		
Val	Glu	Asp	Gly	Thr	Gly	Leu	Glu	Asp	Glu	Leu	Asp	Val	Val	Glu	Gly	
			180					185					190			
Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro	Tyr	Phe	Ile	Asn	Lys	Pro	
		195					200					205				
Glu	Thr	Ala	Gly	Thr	Val	Glu	Leu	Asp	Asn	Pro	Phe	Ile	Leu	Leu	Val	
	210					215					220					
Asp	Lys	Lys	Ile	Ser	Asn	Ile	Arg	Glu	Leu	Leu	Pro	Val	Leu	Glu	Ala	
225					230					235					240	
Val	Ala	Lys	Ala	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	
			245						250					255		
Gly	Glu	Ala	Leu	Ala	Thr	Leu	Val	Val	Asn	Thr	Met	Arg	Gly	Ile	Val	
			260					265					270			
Lys	Val	Ala	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala	
		275					280					285				
Met	Leu	Gln	Asp	Ile	Ala	Ile	Leu	Thr	Ala	Gly	Thr	Val	Ile	Ser	Glu	
	290					295					300					
Glu	Ile	Gly	Met	Glu	Leu	Glu	Lys	Ala	Thr	Leu	Glu	Glu	Leu	Gly	Gln	
305					310					315					320	
Ala	Lys	Arg	Val	Val	Ile	Thr	Lys	Asp	Asn	Thr	Thr	Ile	Ile	Asp	Gly	
			325						330					335		
Ile	Gly	Asp	Glu	Ala	Gln	Ile	Lys	Ala	Arg	Val	Val	Gln	Ile	Arg	Gln	
		340						345					350			
Gln	Ile	Glu	Asp	Ser	Thr	Ser	Asp	Tyr	Asp	Lys	Glu	Lys	Leu	Gln	Glu	
		355					360					365				

Arg Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala  
 370 375 380  
 Ala Thr Glu Val Ala Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala  
 385 390 395 400  
 Leu His Ala Thr Arg Ala Ala Val Glu Glu Gly Ile Val Pro Gly Gly  
 405 410 415  
 Gly Val Ala Leu Val Arg Ala Ala Asn Lys Val Ser Ala Thr Leu Thr  
 420 425 430  
 Gly Asp Asn Glu Glu Gln Asn Val Gly Ile Lys Leu Ala Leu Arg Ala  
 435 440 445  
 Met Glu Ala Pro Leu Arg Gln Ile Val Glu Asn Ser Gly Glu Asp Ala  
 450 455 460  
 Ser Val Val Ala Arg Asp Val Lys Asp Gly Ser Gly Asn Phe Gly Tyr  
 465 470 475 480  
 Asn Ala Thr Thr Glu Glu Tyr Gly Asp Met Leu Glu Met Gly Ile Leu  
 485 490 495  
 Asp Pro Thr Lys Val Thr Arg Ser Ala Leu Gln Phe Ala Ala Ser Ile  
 500 505 510  
 Ala Gly Leu Met Ile Thr Thr Glu Cys Met Ile Thr Asp Leu Pro Lys  
 515 520 525  
 Glu Asp Lys Leu Asp Ala Gln Ala Ala Met Gly Gly Met Gly Gly Met  
 530 535 540  
 Gly Gly Met Met  
 545

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Ala Lys Glu Leu Arg Phe Gly Asp Asp Ala Arg Leu Gln Met Leu  
 1 5 10 15  
 Ala Gly Val Asn Ala Leu Ala Asp Ala Val Gln Val Thr Met Gly Pro  
 20 25 30  
 Arg Gly Arg Asn Val Val Leu Glu Lys Ser Tyr Gly Ala Pro Thr Val

35					40					45					
Thr	Lys	Asp	Gly	Val	Ser	Val	Ala	Lys	Glu	Ile	Glu	Phe	Glu	His	Arg
50					55					60					
Phe	Met	Asn	Met	Gly	Ala	Gln	Met	Val	Lys	Glu	Val	Ala	Ser	Lys	Thr
65					70					75					80
Ser	Asp	Thr	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	Arg
				85					90					95	
Ser	Ile	Leu	Val	Glu	Gly	His	Lys	Ala	Val	Ala	Ala	Gly	Met	Asn	Pro
			100					105					110		
Met	Asp	Leu	Lys	Arg	Gly	Ile	Asp	Lys	Ala	Val	Leu	Ala	Val	Thr	Lys
		115					120					125			
Lys	Leu	Gln	Ala	Met	Ser	Lys	Pro	Cys	Lys	Asp	Ser	Lys	Ala	Ile	Ala
	130					135					140				
Gln	Val	Gly	Thr	Ile	Ser	Ala	Asn	Ser	Asp	Glu	Ala	Ile	Gly	Ala	Ile
145					150					155					160
Ile	Ala	Glu	Ala	Met	Glu	Lys	Val	Gly	Lys	Glu	Gly	Val	Ile	Thr	Val
				165					170					175	
Glu	Asp	Gly	Asn	Gly	Leu	Glu	Asn	Glu	Leu	Ser	Val	Val	Glu	Gly	Met
			180					185					190		
Gln	Phe	Asp	Arg	Gly	Tyr	Ile	Ser	Pro	Tyr	Phe	Ile	Asn	Asn	Gln	Gln
		195					200					205			
Asn	Met	Ser	Cys	Glu	Leu	Glu	His	Pro	Phe	Ile	Leu	Leu	Val	Asp	Lys
	210					215					220				
Lys	Val	Ser	Ser	Ile	Arg	Glu	Met	Leu	Ser	Val	Leu	Glu	Gly	Val	Ala
225					230					235					240
Lys	Ser	Gly	Arg	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	Glu
				245					250					255	
Ala	Leu	Ala	Thr	Leu	Val	Val	Asn	Asn	Met	Arg	Gly	Ile	Val	Lys	Val
			260					265					270		
Cys	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Met	Leu
		275					280					285			
Gln	Asp	Ile	Ala	Ile	Leu	Thr	Lys	Gly	Gln	Val	Ile	Ser	Glu	Glu	Ile
	290					295					300				
Gly	Lys	Ser	Leu	Glu	Gly	Ala	Thr	Leu	Glu	Asp	Leu	Gly	Ser	Ala	Lys
305					310					315					320
Arg	Ile	Val	Val	Thr	Lys	Glu	Asn	Thr	Thr	Ile	Ile	Asp	Gly	Glu	Gly
				325					330					335	
Lys	Ala	Thr	Glu	Ile	Asn	Ala	Arg	Ile	Thr	Gln	Ile	Arg	Ala	Gln	Met
			340					345					350		

Glu Glu Thr Thr Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg Val  
 355 360 365  
 Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Thr  
 370 375 380  
 Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val Glu Asp Ala Leu His  
 385 390 395 400  
 Ala Thr Arg Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Gly Val  
 405 410 415  
 Ala Leu Ile Arg Ala Gln Lys Ala Leu Asp Ser Leu Lys Gly Asp Asn  
 420 425 430  
 Asp Asp Gln Asn Met Gly Ile Asn Ile Leu Arg Arg Ala Ile Glu Ser  
 435 440 445  
 Pro Met Arg Gln Ile Val Thr Asn Ala Gly Tyr Glu Ala Ser Val Val  
 450 455 460  
 Val Asn Lys Val Ala Glu His Lys Asp Asn Tyr Gly Phe Asn Ala Ala  
 465 470 475 480  
 Thr Gly Glu Tyr Gly Asp Met Val Glu Met Gly Ile Leu Asp Pro Thr  
 485 490 495  
 Lys Val Thr Arg Met Ala Leu Gln Asn Ala Ala Ser Val Ala Ser Leu  
 500 505 510  
 Met Leu Thr Thr Glu Cys Met Val Ala Asp Leu Pro Lys Lys Glu Glu  
 515 520 525  
 Gly Val Gly Ala Gly Asp Met Gly Gly Met Gly Gly Met Gly Gly Met  
 530 535 540  
 Gly Gly Met Met Glx  
 545

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg Arg Gly Leu Glu  
 1 5 10 15  
 Arg Gly Leu Asn Ala Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro

20					25					30					
Lys	Gly	Arg	Asn	Val	Val	Leu	Glu	Lys	Lys	Trp	Gly	Ala	Pro	Thr	Ile
	35					40					45				
Thr	Asn	Asp	Gly	Val	Ser	Ile	Ala	Lys	Glu	Ile	Glu	Leu	Glu	Asp	Pro
	50					55					60				
Tyr	Glu	Lys	Ile	Gly	Ala	Glu	Leu	Val	Lys	Glu	Val	Ala	Lys	Lys	Thr
65					70					75					80
Asp	Asp	Val	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	Gln
				85					90					95	
Ala	Leu	Val	Arg	Glu	Gly	Leu	Arg	Asn	Val	Ala	Ala	Gly	Ala	Asn	Pro
			100					105					110		
Leu	Gly	Leu	Lys	Arg	Gly	Ile	Glu	Lys	Ala	Val	Glu	Lys	Val	Thr	Glu
	115						120					125			
Thr	Leu	Leu	Lys	Ser	Ala	Lys	Glu	Val	Glu	Thr	Lys	Asp	Gln	Ile	Ala
	130					135					140				
Ala	Thr	Ala	Ala	Ile	Ser	Ala	Gly	Asp	Gln	Ser	Ile	Gly	Asp	Leu	Ile
145					150					155					160
Ala	Glu	Ala	Met	Asp	Lys	Val	Gly	Asn	Glu	Gly	Val	Ile	Thr	Val	Glu
			165					170						175	
Glu	Ser	Asn	Thr	Phe	Gly	Leu	Gln	Leu	Glu	Leu	Thr	Glu	Gly	Met	Arg
			180					185					190		
Phe	Asp	Lys	Gly	Tyr	Ile	Ser	Gly	Tyr	Phe	Val	Thr	Asp	Ala	Glu	Arg
	195						200					205			
Gln	Glu	Ala	Val	Leu	Glu	Asp	Pro	Phe	Ile	Leu	Leu	Val	Ser	Ser	Lys
	210					215					220				
Val	Ser	Thr	Val	Lys	Asp	Leu	Leu	Pro	Leu	Leu	Glu	Lys	Val	Ile	Gln
225					230					235					240
Ala	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	Glu	Ala
				245					250					255	
Leu	Ser	Thr	Leu	Val	Val	Asn	Lys	Ile	Arg	Gly	Thr	Phe	Lys	Ser	Val
			260					265					270		
Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Met	Leu	Gln
		275					280					285			
Asp	Met	Ala	Ile	Leu	Thr	Gly	Gly	Gln	Val	Ile	Ser	Glu	Glu	Val	Gly
	290					295					300				
Leu	Ser	Leu	Glu	Ser	Ala	Asp	Ile	Ser	Leu	Leu	Gly	Lys	Ala	Arg	Lys
305					310					315					320
Val	Val	Val	Thr	Lys	Asp	Glu	Thr	Thr	Ile	Val	Glu	Gly	Ala	Gly	Asp
				325					330					335	



Ser	Asp	Ala	Ile	Ala	Gly	Arg	Val	Ala	Gln	Ile	Arg	Thr	Glu	Ile	Glu	340	345	350
Asn	Ser	Asp	Ser	Asp	Tyr	Asp	Arg	Glu	Lys	Leu	Gln	Glu	Arg	Leu	Ala	355	360	365
Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Ala	Gly	Ala	Ala	Thr	Glu	370	375	380
Val	Glu	Leu	Lys	Glu	Arg	Lys	His	Arg	Ile	Glu	Asp	Ala	Val	Arg	Asn	385	390	395
Ala	Lys	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Ala	Gly	Gly	Gly	Val	Ala	405	410	415
Leu	Leu	His	Ala	Ile	Pro	Ala	Leu	Asp	Glu	Leu	Lys	Pro	Glu	Gly	Glu	420	425	430
Glu	Ala	Thr	Gly	Ala	Asn	Ile	Val	Arg	Val	Ala	Leu	Glu	Arg	Pro	Leu	435	440	445
Lys	Gln	Ile	Ala	Phe	Asn	Gly	Gly	Leu	Glu	Pro	Gly	Val	Val	Ala	Glu	450	455	460
Lys	Val	Arg	Asn	Ser	Pro	Ala	Gly	Thr	Gly	Leu	Asn	Ala	Ala	Thr	Gly	465	470	475
Glu	Tyr	Glu	Asp	Leu	Leu	Lys	Ala	Gly	Ile	Ala	Asp	Pro	Val	Lys	Val	485	490	495
Thr	Arg	Ser	Ala	Leu	Gln	Asn	Ala	Ala	Ser	Ile	Ala	Gly	Leu	Phe	Leu	500	505	510
Thr	Thr	Glu	Ala	Val	Val	Ala	Asp	Lys	Pro	Glu	Lys	Ala	Ala	Ala	Pro	515	520	525
Ala	Gly	Asp	Pro	Thr	Gly	Gly	Met	Gly	Gly	Met	Asp	Phe				530	535	540

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Ala	Lys	Thr	Ile	Ala	Tyr	Asp	Glu	Glu	Ala	Arg	Arg	Gly	Leu	Glu	1	5	10	15
Arg	Gly	Leu	Asn	Ala	Leu	Ala	Asp	Ala	Val	Lys	Val	Thr	Leu	Gly	Pro				

20					25					30					
Lys	Gly	Arg	Asn	Val	Val	Leu	Glu	Lys	Lys	Trp	Gly	Ala	Pro	Thr	Ile
	35					40					45				
Thr	Asn	Asp	Gly	Val	Ser	Ile	Ala	Lys	Glu	Ile	Glu	Leu	Glu	Asp	Pro
	50					55					60				
Tyr	Glu	Lys	Ile	Gly	Ala	Glu	Leu	Val	Lys	Glu	Val	Ala	Lys	Lys	Thr
65				70					75						80
Asp	Asp	Val	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	Gln
				85					90					95	
Ala	Leu	Val	Arg	Glu	Gly	Leu	Arg	Asn	Val	Ala	Ala	Gly	Ala	Asn	Pro
			100					105					110		
Leu	Gly	Leu	Lys	Arg	Gly	Ile	Glu	Lys	Ala	Val	Glu	Lys	Val	Thr	Glu
	115						120					125			
Thr	Leu	Leu	Lys	Gly	Ala	Lys	Glu	Val	Glu	Thr	Lys	Glu	Gln	Ile	Ala
	130					135					140				
Ala	Thr	Ala	Ala	Ile	Ser	Ala	Gly	Asp	Gln	Ser	Ile	Gly	Asp	Leu	Ile
145				150					155						160
Ala	Glu	Ala	Met	Asp	Lys	Val	Gly	Asn	Glu	Gly	Val	Ile	Thr	Val	Glu
			165					170						175	
Glu	Ser	Asn	Thr	Phe	Gly	Leu	Gln	Leu	Glu	Leu	Thr	Glu	Gly	Met	Arg
			180					185					190		
Phe	Asp	Lys	Gly	Tyr	Ile	Ser	Gly	Tyr	Phe	Val	Thr	Asp	Pro	Glu	Arg
	195						200					205			
Gln	Glu	Ala	Val	Leu	Glu	Asp	Pro	Tyr	Ile	Leu	Leu	Val	Ser	Ser	Lys
	210					215					220				
Val	Ser	Thr	Val	Lys	Asp	Leu	Leu	Pro	Leu	Leu	Glu	Lys	Val	Ile	Gly
225				230					235						240
Ala	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	Glu	Ala
				245				250						255	
Leu	Ser	Thr	Leu	Val	Val	Asn	Lys	Ile	Arg	Gly	Thr	Phe	Lys	Ser	Val
			260					265					270		
Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Met	Leu	Gln
	275						280					285			
Asp	Met	Ala	Ile	Leu	Thr	Gly	Gly	Gln	Val	Ile	Ser	Glu	Glu	Val	Gly
	290					295					300				
Leu	Thr	Leu	Glu	Asn	Ala	Asp	Leu	Ser	Leu	Leu	Gly	Lys	Ala	Arg	Lys
305				310					315						320
Val	Val	Val	Thr	Lys	Asp	Glu	Thr	Thr	Ile	Val	Glu	Gly	Ala	Gly	Asp
				325					330					335	

Thr	Asp	Ala	Ile	Ala	Gly	Arg	Val	Ala	Gln	Ile	Arg	Gln	Glu	Ile	Glu	340	345	350	
Asn	Ser	Asp	Ser	Asp	Tyr	Asp	Arg	Glu	Lys	Leu	Gln	Glu	Arg	Leu	Ala	355	360	365	
Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Ala	Gly	Ala	Ala	Thr	Glu	370	375	380	
Val	Glu	Leu	Lys	Glu	Arg	Lys	His	Arg	Ile	Glu	Asp	Ala	Val	Arg	Asn	385	390	395	400
Ala	Lys	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Ala	Gly	Gly	Gly	Val	Thr	405	410	415	
Leu	Leu	Gln	Ala	Ala	Pro	Thr	Leu	Asp	Glu	Leu	Lys	Leu	Glu	Gly	Asp	420	425	430	
Glu	Ala	Thr	Gly	Ala	Asn	Ile	Val	Lys	Val	Ala	Leu	Glu	Ala	Pro	Leu	435	440	445	
Lys	Gln	Ile	Ala	Phe	Asn	Ser	Gly	Leu	Glu	Pro	Gly	Val	Val	Ala	Glu	450	455	460	
Lys	Val	Arg	Asn	Leu	Pro	Ala	Gly	His	Gly	Leu	Asn	Ala	Gln	Thr	Gly	465	470	475	480
Val	Tyr	Glu	Asp	Leu	Leu	Ala	Ala	Gly	Val	Ala	Asp	Pro	Val	Lys	Val	485	490	495	
Thr	Arg	Ser	Ala	Leu	Gln	Asn	Ala	Ala	Ser	Ile	Ala	Gly	Leu	Phe	Leu	500	505	510	
Thr	Thr	Glu	Ala	Val	Val	Ala	Asp	Lys	Pro	Glu	Lys	Glu	Lys	Ala	Ser	515	520	525	
Val	Pro	Gly	Gly	Gly	Asp	Met	Gly	Gly	Met	Asp	Phe	530	535	540					

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	Ser	Lys	Leu	Ile	Glu	Tyr	Asp	Glu	Thr	Ala	Arg	His	Ala	Met	Glu	1	5	10	15
Val	Gly	Met	Asn	Lys	Leu	Ala	Asp	Thr	Val	Arg	Val	Thr	Leu	Gly	Pro				

20					25					30					
Arg	Gly	Arg	His	Val	Val	Leu	Ala	Lys	Ala	Phe	Gly	Gly	Pro	Thr	Ile
	35						40					45			
Thr	Asn	Asp	Gly	Val	Thr	Val	Ala	Arg	Glu	Ile	Asp	Leu	Glu	Asp	Pro
	50					55					60				
Phe	Glu	Asn	Leu	Gly	Ala	Gln	Leu	Val	Lys	Ser	Val	Ala	Thr	Lys	Thr
65					70					75					80
Asn	Asp	Val	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	Gln
				85					90					95	
Ala	Leu	Val	Lys	Gly	Gly	Leu	Arg	Met	Val	Ala	Ala	Gly	Ala	Asn	Pro
			100					105					110		
Val	Ala	Leu	Gly	Ala	Gly	Ile	Ser	Lys	Ala	Ala	Asp	Ala	Val	Ser	Glu
		115					120					125			
Ala	Leu	Leu	Ala	Val	Ala	Thr	Pro	Val	Ala	Gly	Lys	Asp	Ala	Ile	Thr
	130					135						140			
Gln	Val	Ala	Thr	Val	Ser	Ser	Arg	Asp	Glu	Gln	Ile	Gly	Ala	Leu	Val
145					150					155					160
Gly	Glu	Gly	Met	Asn	Lys	Val	Gly	Thr	Asp	Gly	Val	Val	Ser	Val	Glu
				165					170					175	
Glu	Ser	Ser	Thr	Leu	Asp	Thr	Glu	Leu	Glu	Phe	Thr	Glu	Gly	Val	Gly
			180					185					190		
Phe	Asp	Lys	Gly	Phe	Leu	Ser	Ala	Tyr	Phe	Val	Thr	Asp	Phe	Asp	Ser
		195					200					205			
Gln	Gln	Ala	Val	Leu	Asp	Asp	Pro	Leu	Val	Leu	Leu	His	Gln	Glu	Lys
	210					215					220				
Ile	Ser	Ser	Leu	Pro	Glu	Leu	Leu	Pro	Met	Leu	Glu	Lys	Val	Thr	Glu
225					230					235					240
Ser	Gly	Lys	Pro	Leu	Leu	Ile	Val	Ala	Glu	Asp	Leu	Glu	Gly	Glu	Ala
				245					250					255	
Leu	Ala	Thr	Leu	Val	Val	Asn	Ser	Ile	Arg	Lys	Thr	Leu	Lys	Ala	Val
			260					265					270		
Ala	Val	Lys	Ser	Pro	Phe	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Phe	Leu	Glu
		275					280					285			
Asp	Leu	Ala	Ile	Val	Thr	Gly	Gly	Gln	Val	Val	Asn	Pro	Glu	Thr	Gly
	290					295					300				
Leu	Val	Leu	Arg	Glu	Val	Gly	Thr	Asp	Val	Leu	Gly	Ser	Ala	Arg	Arg
305					310					315					320
Val	Val	Val	Ser	Lys	Asp	Asp	Thr	Ile	Ile	Val	Asp	Gly	Gly	Gly	Ser
				325					330					335	

Asn	Asp	Ala	Val	Ala	Lys	Arg	Val	Asn	Gln	Leu	Arg	Ala	Glu	Ile	Glu	340	345	350	
Val	Ser	Asp	Ser	Glu	Trp	Asp	Arg	Glu	Lys	Leu	Gln	Glu	Arg	Val	Ala	355	360	365	
Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	Ala	Val	Thr	Glu	370	375	380	
Thr	Ala	Leu	Lys	Lys	Arg	Lys	Glu	Ser	Val	Glu	Asp	Ala	Val	Ala	Ala	385	390	395	400
Ala	Lys	Ala	Ser	Ile	Glu	Glu	Gly	Ile	Ile	Ala	Gly	Gly	Gly	Ser	Ala	405	410	415	
Leu	Val	Gln	Cys	Gly	Ala	Ala	Leu	Lys	Gln	Leu	Arg	Thr	Ser	Leu	Thr	420	425	430	
Gly	Asp	Glu	Ala	Leu	Gly	Ile	Asp	Val	Phe	Phe	Glu	Ala	Leu	Lys	Ala	435	440	445	
Pro	Leu	Tyr	Trp	Ile	Ala	Thr	Asn	Ala	Gly	Leu	Asp	Gly	Ala	Val	Val	450	455	460	
Val	Asp	Lys	Val	Ser	Gly	Leu	Pro	Ala	Gly	His	Gly	Leu	Asn	Ala	Ser	465	470	475	480
Thr	Leu	Gly	Tyr	Gly	Asp	Leu	Val	Ala	Asp	Gly	Val	Val	Asp	Pro	Val	485	490	495	
Lys	Val	Thr	Arg	Ser	Ala	Val	Leu	Asn	Ala	Ala	Ser	Val	Ala	Arg	Met	500	505	510	
Met	Leu	Thr	Thr	Glu	Thr	Ala	Val	Val	Asp	Lys	Pro	Ala	Lys	Thr	Glu	515	520	525	
Glu	His	Asp	His	His	Gly	His	Ala	His								530	535		

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Ala	Lys	Thr	Ile	Ala	Tyr	Asp	Glu	Glu	Ala	Arg	Arg	Gly	Leu	Glu	1	5	10	15
Arg	Gly	Leu	Asn	Ser	Leu	Ala	Asp	Ala	Val	Lys	Val	Thr	Leu	Gly	Pro				

20					25					30					
Lys	Gly	Arg	Asn	Val	Val	Leu	Glu	Lys	Lys	Trp	Gly	Ala	Pro	Thr	Ile
	35					40					45				
Thr	Asn	Asp	Gly	Val	Ser	Ile	Ala	Lys	Glu	Ile	Glu	Leu	Glu	Asp	Pro
	50					55					60				
Tyr	Glu	Lys	Ile	Gly	Ala	Glu	Leu	Val	Lys	Glu	Val	Ala	Lys	Lys	Thr
65				70					75						80
Asp	Asp	Val	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	Gln
				85					90					95	
Ala	Leu	Val	Lys	Glu	Gly	Leu	Arg	Asn	Val	Ala	Ala	Gly	Ala	Asn	Pro
			100					105					110		
Leu	Gly	Leu	Lys	Arg	Gly	Ile	Glu	Lys	Ala	Val	Asp	Lys	Val	Thr	Glu
	115						120					125			
Thr	Leu	Leu	Lys	Asp	Ala	Lys	Glu	Val	Glu	Thr	Lys	Glu	Gln	Ile	Ala
	130					135					140				
Ala	Thr	Ala	Ala	Ile	Ser	Ala	Gly	Asp	Gln	Ser	Ile	Gly	Asp	Leu	Ile
145				150					155						160
Ala	Glu	Ala	Met	Asp	Lys	Val	Gly	Met	Glu	Gly	Val	Ile	Thr	Val	Glu
			165					170						175	
Glu	Ser	Asn	Thr	Phe	Gly	Leu	Gln	Leu	Glu	Leu	Thr	Glu	Gly	Met	Arg
			180				185						190		
Phe	Asp	Lys	Gly	Tyr	Ile	Ser	Gly	Tyr	Phe	Val	Thr	Asp	Ala	Glu	Arg
	195						200					205			
Gln	Glu	Ala	Val	Leu	Glu	Glu	Pro	Tyr	Ile	Leu	Leu	Val	Ser	Ser	Lys
	210					215					220				
Val	Ser	Thr	Val	Lys	Asp	Leu	Leu	Pro	Leu	Leu	Glu	Lys	Val	Ile	Gln
225				230					235						240
Ala	Gly	Lys	Ser	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	Glu	Ala
				245				250						255	
Leu	Ser	Thr	Leu	Val	Val	Asn	Lys	Ile	Arg	Gly	Thr	Phe	Lys	Ser	Val
			260				265						270		
Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Met	Leu	Gln
	275						280					285			
Asp	Met	Ala	Ile	Leu	Thr	Gly	Ala	Gln	Val	Ile	Ser	Glu	Glu	Val	Gly
	290					295					300				
Leu	Thr	Leu	Glu	Asn	Thr	Asp	Leu	Ser	Leu	Leu	Gly	Lys	Ala	Arg	Lys
305				310					315						320
Val	Val	Met	Thr	Lys	Asp	Glu	Thr	Thr	Ile	Val	Glu	Gly	Ala	Gly	Asp
				325					330					335	

Thr	Asp	Ala	Ile	Ala	Gly	Arg	Val	Ala	Gln	Ile	Arg	Thr	Glu	Ile	Glu	340	345	350
Asn	Ser	Asp	Ser	Asp	Tyr	Asp	Arg	Glu	Lys	Leu	Gln	Glu	Arg	Leu	Ala	355	360	365
Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Ala	Gly	Ala	Ala	Thr	Glu	370	375	380
Val	Glu	Leu	Lys	Glu	Arg	Lys	His	Arg	Ile	Glu	Asp	Ala	Val	Arg	Asn	385	390	395
Ala	Lys	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Ala	Gly	Gly	Gly	Val	Thr	405	410	415
Leu	Leu	Gln	Ala	Ala	Pro	Ala	Leu	Asp	Lys	Leu	Lys	Leu	Thr	Gly	Asp	420	425	430
Glu	Ala	Thr	Gly	Ala	Asn	Ile	Val	Lys	Val	Ala	Leu	Glu	Ala	Pro	Leu	435	440	445
Lys	Gln	Ile	Ala	Phe	Asn	Ser	Gly	Met	Glu	Pro	Gly	Val	Val	Ala	Glu	450	455	460
Lys	Val	Arg	Asn	Leu	Ser	Val	Gly	His	Gly	Leu	Asn	Ala	Ala	Thr	Gly	465	470	475
Glu	Tyr	Glu	Asp	Leu	Leu	Lys	Ala	Gly	Val	Ala	Asp	Pro	Val	Lys	Val	485	490	495
Thr	Arg	Ser	Ala	Leu	Gln	Asn	Ala	Ala	Ser	Ile	Ala	Gly	Leu	Phe	Leu	500	505	510
Thr	Thr	Glu	Ala	Val	Val	Ala	Asp	Lys	Pro	Glu	Lys	Thr	Ala	Ala	Pro	515	520	525
Ala	Ser	Asp	Pro	Thr	Gly	Gly	Met	Gly	Gly	Met	Asp	Phe				530	535	540

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Ser	Lys	Leu	Ile	Glu	Tyr	Asp	Glu	Thr	Ala	Arg	Arg	Ala	Met	Glu	1	5	10	15
Val	Gly	Met	Asp	Lys	Leu	Ala	Asp	Thr	Val	Arg	Val	Thr	Leu	Gly	Pro				

20					25					30					
Arg	Gly	Arg	His	Val	Val	Leu	Ala	Lys	Ala	Phe	Gly	Gly	Pro	Thr	Val
	35						40					45			
Thr	Asn	Asp	Gly	Val	Thr	Val	Ala	Arg	Glu	Ile	Glu	Leu	Glu	Asp	Pro
	50					55					60				
Phe	Glu	Asp	Leu	Gly	Ala	Gln	Leu	Val	Lys	Ser	Val	Ala	Thr	Lys	Thr
65					70					75					80
Asn	Asp	Val	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Ile	Leu	Ala	Gln
				85					90					95	
Ala	Leu	Ile	Lys	Gly	Gly	Leu	Arg	Leu	Val	Ala	Ala	Gly	Val	Asn	Pro
			100					105					110		
Ile	Ala	Leu	Gly	Val	Gly	Ile	Gly	Lys	Ala	Ala	Asp	Ala	Val	Ser	Glu
	115						120					125			
Ala	Leu	Leu	Ala	Ser	Ala	Thr	Pro	Val	Ser	Gly	Lys	Thr	Gly	Ile	Ala
	130					135						140			
Gln	Val	Ala	Thr	Val	Ser	Ser	Arg	Asp	Glu	Gln	Ile	Gly	Asp	Leu	Val
145						150					155				160
Gly	Glu	Ala	Met	Ser	Lys	Val	Gly	His	Asp	Gly	Val	Val	Ser	Val	Glu
				165					170					175	
Glu	Ser	Ser	Thr	Leu	Gly	Thr	Glu	Leu	Glu	Phe	Thr	Glu	Gly	Ile	Gly
			180					185					190		
Phe	Asp	Lys	Gly	Phe	Leu	Ser	Ala	Tyr	Phe	Val	Thr	Asp	Phe	Asp	Asn
		195					200					205			
Gln	Gln	Ala	Val	Leu	Glu	Asp	Ala	Leu	Ile	Leu	Leu	His	Gln	Asp	Lys
	210					215						220			
Ile	Ser	Ser	Leu	Pro	Asp	Leu	Leu	Pro	Leu	Leu	Glu	Lys	Val	Ala	Gly
225						230					235				240
Thr	Gly	Lys	Pro	Leu	Leu	Ile	Val	Ala	Glu	Asp	Val	Glu	Gly	Glu	Ala
				245					250					255	
Leu	Ala	Thr	Leu	Val	Val	Asn	Ala	Ile	Arg	Lys	Thr	Leu	Lys	Ala	Val
			260					265					270		
Ala	Val	Lys	Gly	Pro	Tyr	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Phe	Leu	Glu
		275					280					285			
Asp	Leu	Ala	Val	Val	Thr	Gly	Gly	Gln	Val	Val	Asn	Pro	Asp	Ala	Gly
	290					295					300				
Met	Val	Leu	Arg	Glu	Val	Gly	Leu	Glu	Val	Leu	Gly	Ser	Ala	Arg	Arg
305						310					315				320
Val	Val	Val	Ser	Lys	Asp	Asp	Thr	Val	Ile	Val	Asp	Gly	Gly	Gly	Thr
				325					330					335	



Ala	Glu	Ala	Val	Ala	Asn	Arg	Ala	Lys	His	Leu	Arg	Ala	Glu	Ile	Asp	340	345	350
Lys	Ser	Asp	Ser	Asp	Trp	Asp	Arg	Glu	Lys	Leu	Gly	Glu	Arg	Leu	Ala	355	360	365
Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	Ala	Ala	Thr	Glu	370	375	380
Thr	Ala	Leu	Lys	Glu	Arg	Lys	Glu	Ser	Val	Glu	Asp	Ala	Val	Ala	Ala	385	390	395
Ala	Lys	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Pro	Gly	Gly	Gly	Ala	Ser	405	410	415
Leu	Ile	His	Gln	Ala	Arg	Lys	Ala	Leu	Thr	Glu	Leu	Arg	Ala	Ser	Leu	420	425	430
Thr	Gly	Asp	Glu	Val	Leu	Gly	Val	Asp	Val	Phe	Ser	Glu	Ala	Leu	Ala	435	440	445
Ala	Pro	Leu	Phe	Trp	Ile	Ala	Ala	Asn	Ala	Gly	Leu	Asp	Gly	Ser	Val	450	455	460
Val	Val	Lys	Lys	Val	Ser	Glu	Leu	Pro	Ala	Gly	His	Gly	Leu	Asn	Val	465	470	475
Asn	Thr	Leu	Ser	Tyr	Gly	Asp	Leu	Ala	Ala	Asp	Gly	Val	Ile	Asp	Pro	485	490	495
Val	Lys	Val	Thr	Arg	Ser	Ala	Val	Leu	Asn	Ala	Ser	Ser	Val	Ala	Arg	500	505	510
Met	Val	Leu	Thr	Thr	Glu	Thr	Val	Val	Val	Asp	Lys	Pro	Ala	Lys	Ala	515	520	525
Glu	Asp	His	Asp	His	His	His	Gly	His	Ala	His						530	535	

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Ala	Ala	Lys	Asp	Val	Gln	Phe	Gly	Asn	Glu	Val	Arg	Gln	Lys	Met	1	5	10	15
Val	Asn	Gly	Val	Asn	Ile	Leu	Ala	Asn	Ala	Val	Arg	Val	Thr	Leu	Gly				

20					25					30					
Pro	Lys	Gly	Arg	Asn	Val	Val	Val	Asp	Arg	Ala	Phe	Gly	Gly	Pro	His
		35					40					45			
Ile	Thr	Lys	Asp	Gly	Val	Thr	Val	Ala	Lys	Glu	Ile	Glu	Leu	Lys	Asp
	50					55					60				
Lys	Phe	Glu	Asn	Met	Gly	Ala	Gln	Met	Val	Lys	Glu	Val	Ala	Ser	Lys
65					70					75					80
Thr	Asn	Asp	Val	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala
				85					90					95	
Gln	Ser	Ile	Val	Ala	Glu	Gly	Met	Lys	Tyr	Val	Thr	Ala	Gly	Met	Asn
			100					105					110		
Pro	Thr	Asp	Leu	Lys	Arg	Gly	Ile	Asp	Lys	Ala	Val	Ala	Ala	Leu	Val
		115					120					125			
Glu	Glu	Leu	Lys	Asn	Ile	Ala	Lys	Pro	Cys	Asp	Thr	Ser	Lys	Glu	Ile
	130					135					140				
Ala	Gln	Val	Gly	Ser	Ile	Ser	Ala	Asn	Ser	Asp	Glu	Gln	Val	Gly	Ala
145					150					155					160
Ile	Ile	Ala	Glu	Ala	Met	Glu	Lys	Val	Gly	Lys	Glu	Gly	Val	Ile	Thr
				165					170					175	
Val	Glu	Asp	Gly	Lys	Ser	Leu	Glu	Asn	Glu	Leu	Asp	Val	Val	Glu	Gly
			180					185					190		
Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro	Tyr	Phe	Ile	Asn	Asp	Ala
		195					200					205			
Glu	Lys	Gln	Ile	Ala	Gly	Leu	Asp	Asn	Pro	Phe	Val	Leu	Leu	Phe	Asp
	210					215					220				
Lys	Lys	Ile	Ser	Asn	Ile	Arg	Asp	Leu	Leu	Pro	Val	Leu	Glu	Gln	Val
225					230					235					240
Ala	Lys	Ala	Ser	Arg	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly
				245					250					255	
Glu	Ala	Leu	Ala	Thr	Leu	Val	Val	Asn	Asn	Ile	Arg	Gly	Ile	Leu	Lys
			260					265					270		
Thr	Val	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Met
		275					280					285			
Leu	Gln	Asp	Ile	Ala	Ile	Leu	Thr	Gly	Gly	Thr	Val	Ile	Ser	Glu	Glu
	290					295					300				
Val	Gly	Leu	Ser	Leu	Glu	Lys	Ala	Thr	Leu	Asp	Asp	Leu	Gly	Gln	Ala
305					310					315					320
Lys	Arg	Ile	Glu	Ile	Gly	Lys	Glu	Asn	Thr	Thr	Ile	Ile	Asp	Gly	Phe
				325					330					335	

Gly	Asp	Ala	Ala	Gln	Ile	Glu	Ala	Arg	Val	Ala	Glu	Ile	Arg	Gln	Gln	340	345	350
Ile	Glu	Thr	Ala	Thr	Ser	Asp	Tyr	Asp	Lys	Glu	Lys	Leu	Gln	Glu	Arg	355	360	365
Val	Ala	Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	Ala	Ala	370	375	380
Thr	Glu	Val	Glu	Met	Lys	Glu	Lys	Lys	Asp	Arg	Val	Glu	Asp	Ala	Leu	385	390	395
His	Ala	Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	Val	Val	Ala	Gly	Gly	Gly	405	410	415
Val	Ala	Leu	Leu	Arg	Ala	Arg	Ala	Ala	Leu	Glu	Asn	Leu	His	Thr	Gly	420	425	430
Asn	Ala	Asp	Gln	Asp	Ala	Gly	Val	Gln	Ile	Val	Leu	Arg	Ala	Val	Glu	435	440	445
Ser	Pro	Leu	Arg	Gln	Ile	Val	Ala	Asn	Ala	Gly	Gly	Glu	Pro	Ser	Val	450	455	460
Val	Val	Asn	Lys	Val	Leu	Glu	Gly	Lys	Gly	Asn	Tyr	Gly	Tyr	Asn	Ala	465	470	475
Gly	Ser	Gly	Glu	Tyr	Gly	Asp	Met	Ile	Glu	Met	Gly	Val	Leu	Asp	Pro	485	490	495
Ala	Lys	Val	Thr	Arg	Ser	Ala	Leu	Gln	His	Ala	Ala	Ser	Ile	Ala	Gly	500	505	510
Leu	Met	Leu	Thr	Thr	Asp	Cys	Met	Ile	Ala	Glu	Ile	Pro	Glu	Glu	Lys	515	520	525
Pro	Ala	Met	Pro	Asp	Met	Gly	Gly	Met	Gly	Gly	Met	Gly	Gly	Met	Met	530	535	540
Glx																545		

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Val Lys Gln Leu Lys Phe Ser Glu Asp Ala Arg Gln Ala Met Leu

1	5	10	15
Arg Gly Val	Asp Gln Leu	Ala Asn Ala	Val Lys Val Thr Ile Gly Pro
	20	25	30
Lys Gly Arg	Asn Val Val	Leu Asp Lys	Glu Phe Thr Ala Pro Leu Ile
	35	40	45
Thr Asn Asp	Gly Val Thr	Ile Ala Lys	Glu Ile Glu Leu Glu Asp Pro
	50	55	60
Tyr Glu Asn	Met Gly Ala	Lys Leu Val	Gln Glu Val Ala Asn Lys Thr
65		70	75
Asn Glu Ile	Ala Gly Asp	Gly Thr Thr	Thr Ala Thr Val Leu Ala Gln
	85	90	95
Ala Met Ile	Gln Glu Gly	Leu Lys Asn	Val Thr Ser Gly Ala Asn Pro
	100	105	110
Val Gly Leu	Arg Gln Gly	Ile Asp Lys	Ala Val Lys Val Ala Val Glu
	115	120	125
Ala Leu His	Glu Asn Ser	Gln Lys Val	Glu Asn Lys Asn Glu Ile Ala
	130	135	140
Gln Val Gly	Ala Ile Ser	Ala Ala Asp	Glu Glu Ile Gly Arg Tyr Ile
145		150	155
Ser Glu Ala	Thr Glu Lys	Val Gly Asn	Asp Gly Val Ile Thr Ile Ile
	165	170	175
Thr Ile Glu	Glu Ser Asn	Arg Leu Asn	Thr Glu Leu Glu Leu Gly Met
	180	185	190
Gln Phe Asp	Arg Gly Tyr	Gln Ser Pro	Tyr Met Val Thr Asp Ser Asp
	195	200	205
Lys Met Val	Ala Glu Leu	Glu Arg Pro	Tyr Ile Leu Val Thr Asp Lys
	210	215	220
Lys Ile Ser	Ser Phe Gln	Asp Ile Leu	Pro Leu Leu Glu Gln Val Val
225		230	235
Gln Ser Asn	Arg Pro Ile	Leu Ile Val	Ala Asp Glu Val Glu Gly Asp
	245	250	255
Ala Leu Thr	Asn Ile Val	Leu Asn Arg	Met Arg Gly Thr Phe Thr Ala
	260	265	270
Val Ala Val	Lys Ala Pro	Gly Phe Gly	Asp Arg Arg Lys Ala Met Leu
	275	280	285
Glu Asp Leu	Ala Ile Leu	Thr Gly Ala	Gln Val Ile Thr Asp Asp Leu
	290	295	300
Gly Leu Asp	Leu Lys Asp	Ala Ser Ile	Asp Met Leu Gly Thr Ala Ser
305		310	315
			320

Lys	Val	Glu	Val	Thr	Lys	Asp	Asn	Thr	Thr	Val	Val	Asp	Gly	Asp	Gly	325	330	335	
Asp	Glu	Asn	Ser	Ile	Asp	Ala	Arg	Val	Ser	Gln	Leu	Lys	Ser	Gln	Ile	340	345	350	
Glu	Glu	Thr	Glu	Ser	Asp	Phe	Asp	Arg	Glu	Lys	Leu	Gln	Glu	Arg	Leu	355	360	365	
Ala	Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	Ala	Ala	Ser	370	375	380	
Glu	Thr	Glu	Leu	Lys	Glu	Arg	Lys	Leu	Arg	Ile	Glu	Asp	Ala	Leu	Asn	385	390	395	400
Ser	Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Ala	Gly	Gly	Gly	Thr	405	410	415	
Ala	Leu	Val	Asn	Val	Tyr	Gln	Lys	Val	Ser	Glu	Asn	Glu	Ala	Glu	Gly	420	425	430	
Asp	Ile	Glu	Thr	Gly	Val	Asn	Ile	Val	Leu	Lys	Ala	Leu	Thr	Ala	Pro	435	440	445	
Val	Arg	Gln	Ile	Ala	Glu	Asn	Ala	Gly	Leu	Glu	Gly	Ser	Val	Ile	Val	450	455	460	
Glu	Arg	Leu	Lys	Asn	Ala	Glu	Pro	Gly	Val	Gly	Phe	Asn	Gly	Ala	Thr	465	470	475	480
Asn	Glu	Trp	Val	Asn	Met	Leu	Arg	Arg	Gly	Ile	Val	Asp	Pro	Thr	Lys	485	490	495	
Val	Thr	Arg	Ser	Ala	Leu	Gln	His	Ala	Ala	Ser	Val	Ala	Ala	Met	Phe	500	505	510	
Leu	Thr	Thr	Glu	Ala	Val	Val	Ala	Ser	Ile	Pro	Glu	Lys	Asn	Asn	Asp	515	520	525	
Gln	Pro	Asn	Met	Gly	Gly	Met	Pro	Gly	Met	Met						530	535		

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ala Lys Ser Ile Ile Tyr Asn Asp Glu Ala Arg Arg Ala Leu Glu

1	5	10	15
Arg Gly Met Asp Ile Leu Ala Glu Ala Val Ala Val Thr Leu Gly Pro	20	25	30
Lys Gly Arg Asn Val Val Leu Glu Lys Lys Phe Gly Ser Pro Gln Ile	35	40	45
Ile Asn Asp Gly Ile Thr Ile Ala Lys Glu Ile Glu Leu Glu Asp His	50	55	60
Val Glu Asn Thr Gly Val Ser Leu Ile Arg Gln Ala Ala Ser Lys Thr	65	70	75
Asn Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala His	85	90	95
Ala Ile Val Lys Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro	100	105	110
Ile Ser Leu Lys Arg Gly Ile Asp Lys Ala Thr Asp Phe Leu Val Ala	115	120	125
Arg Ile Lys Glu His Ala Gln Pro Val Gly Asp Ser Lys Ala Ile Ala	130	135	140
Gln Val Gly Ala Ile Ser Ala Gly Asn Asp Glu Glu Val Gly Gln Met	145	150	155
Ile Ala Asn Ala Met Asp Lys Val Gly Gln Glu Gly Val Ile Ser Leu	165	170	175
Glu Glu Gly Lys Ser Met Thr Thr Glu Leu Glu Ile Thr Glu Gly Met	180	185	190
Arg Phe Asp Lys Gly Tyr Ile Ser Pro Tyr Phe Val Thr Asp Ala Glu	195	200	205
Arg Met Glu Ala Val Leu Glu Asp Pro Arg Ile Leu Ile Thr Asp Lys	210	215	220
Lys Ile Asn Leu Val Gln Asp Leu Val Pro Ile Leu Glu Gln Val Ala	225	230	235
Arg Gln Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Ile Glu Lys Glu	245	250	255
Ala Leu Ala Thr Leu Val Val Asn Arg Leu Arg Gly Val Leu Asn Val	260	265	270
Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Gln Met Leu	275	280	285
Glu Asp Ile Ala Thr Leu Thr Gly Gly Gln Val Ile Ser Glu Asp Ala	290	295	300
Gly Leu Lys Leu Glu Ser Ala Thr Val Asp Ser Leu Gly Ser Ala Arg	305	310	315
			320

Arg	Ile	Asn	Ile	Thr	Lys	Asp	Asn	Thr	Thr	Ile	Val	Ala	Glu	Gly	Asn	
				325					330						335	
Glu	Ala	Ala	Val	Lys	Ser	Arg	Cys	Glu	Gln	Ile	Arg	Arg	Gln	Ile	Glu	
			340					345					350			
Glu	Thr	Asp	Ser	Ser	Tyr	Asp	Lys	Glu	Lys	Leu	Gln	Glu	Arg	Leu	Ala	
		355					360					365				
Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	Ala	Ala	Thr	Glu	
	370					375					380					
Thr	Glu	Met	Lys	Asp	Arg	Lys	Leu	Arg	Leu	Glu	Asp	Ala	Ile	Asn	Ala	
385					390					395					400	
Thr	Lys	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Pro	Gly	Gly	Gly	Thr	Thr	
				405					410					415		
Leu	Ala	His	Leu	Ala	Pro	Gln	Leu	Glu	Asp	Trp	Ala	Thr	Gly	Asn	Leu	
			420					425					430			
Lys	Asp	Glu	Glu	Leu	Thr	Gly	Ala	Leu	Ile	Val	Ala	Arg	Ala	Leu	Pro	
	435						440					445				
Ala	Pro	Leu	Lys	Arg	Ile	Ala	Glu	Asn	Ala	Gly	Gln	Asn	Gly	Ala	Val	
	450					455					460					
Ile	Ser	Glu	Arg	Val	Lys	Glu	Lys	Glu	Phe	Asn	Val	Gly	Tyr	Asn	Ala	
465					470					475					480	
Ala	Ser	Leu	Glu	Tyr	Val	Asp	Met	Leu	Ala	Ala	Gly	Ile	Val	Asp	Pro	
				485				490						495		
Ala	Lys	Val	Thr	Arg	Ser	Ala	Leu	Gln	Asn	Ala	Ala	Ser	Ile	Ala	Gly	
			500					505					510			
Met	Val	Leu	Thr	Thr	Glu	Cys	Ile	Val	Val	Asp	Lys	Pro	Glu	Lys	Glu	
		515					520					525				
Lys	Ala	Pro	Ala	Gly	Ala	Pro	Gly	Gly	Asp	Phe	Asp	Tyr				
	530					535					540					

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Ser Lys Leu Ile Ser Phe Lys Asp Glu Ser Arg Arg Ser Leu Glu

1	5	10	15
Ala Gly Ile	Asn Ala Leu Ala Asp	Ala Val Arg Ile Thr	Leu Gly Pro
	20	25	30
Lys Gly Arg	Asn Val Leu Leu Glu	Lys Gln Tyr Gly	Ala Pro Gln Ile
	35	40	45
Val Asn Asp	Gly Ile Thr Val Ala Lys	Glu Ile Glu Leu Ser	Asn Pro
	50	55	60
Glu Glu Asn	Ala Gly Ala Lys Leu Ile	Gln Glu Val Ala Ser	Lys Thr
	65	70	75
Lys Glu Ile	Ala Gly Asp Gly Thr Thr	Thr Ala Thr Ile Ile	Ala Gln
	85	90	95
Ala Leu Val	Arg Glu Gly Leu Arg Asn	Val Ala Ala Gly	Ala Asn Pro
	100	105	110
Val Ala Leu	Arg Arg Gly Ile Glu Lys	Val Thr Thr Phe	Leu Val Gln
	115	120	125
Glu Ile Glu	Ala Val Ala Lys Pro Val	Glu Gly Ser Ala Ile	Ala Gln
	130	135	140
Val Ala Thr	Val Ser Ser Gly Asn Asp	Pro Glu Val Gly	Ala Met Ile
	145	150	155
Ala Asp Ala	Met Asp Lys Val Thr Lys	Asp Gly Val Ile Thr	Val Glu
	165	170	175
Glu Ser Lys	Ser Leu Asn Thr Glu Leu	Glu Val Val Glu Gly	Met Gln
	180	185	190
Ile Asp Arg	Gly Tyr Ile Ser Pro Tyr	Phe Ile Thr Asp	Ser Asp Arg
	195	200	205
Gln Leu Val	Glu Phe Asp Asn Pro Leu	Ile Leu Ile Thr Asp	Lys Lys
	210	215	220
Ile Ser Ala	Ile Ala Glu Leu Val Pro	Val Leu Glu Ala Val	Ala Arg
	225	230	235
Ala Gly Arg	Pro Leu Leu Ile Ile Ala	Glu Asp Ile Glu Gly	Glu Ala
	245	250	255
Leu Ala Thr	Leu Val Val Asn Lys Ala	Arg Gly Val Leu Asn	Val Ala
	260	265	270
Ala Ile Lys	Ala Pro Ala Phe Gly Asp	Arg Arg Lys Ala Val	Leu Gln
	275	280	285
Asp Ile Ala	Ile Leu Thr Gly Gly Ser	Val Ile Ser Glu Asp	Ile Gly
	290	295	300
Leu Ser Leu	Asp Thr Val Ser Leu Asp	Gln Leu Gly Gln Ala	Val Lys
	305	310	315
			320



Ala	Thr	Leu	Glu	Lys	Asp	Asn	Thr	Ile	Leu	Val	Ala	Gly	Ala	Asp	Lys	325	330	335	
Arg	Ala	Ser	Ala	Gly	Val	Lys	Glu	Arg	Ile	Glu	Gln	Leu	Arg	Lys	Glu	340	345	350	
Tyr	Ala	Ala	Ser	Asp	Ser	Asp	Tyr	Asp	Lys	Glu	Lys	Ile	Gln	Glu	Arg	355	360	365	
Ile	Ala	Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	Ala	Ala	370	375	380	
Thr	Glu	Thr	Glu	Leu	Lys	Asp	Arg	Lys	Leu	Arg	Ile	Glu	Asp	Ala	Leu	385	390	395	400
Asn	Ala	Thr	Lys	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Pro	Gly	Gly	Gly	405	410	415	
Thr	Thr	Leu	Ile	Arg	Leu	Ala	Gly	Lys	Ile	Glu	Ser	Phe	Lys	Ala	Gln	420	425	430	
Leu	Ser	Asn	Asp	Glu	Glu	Arg	Val	Ala	Ala	Asp	Ile	Ile	Ala	Lys	Ala	435	440	445	
Leu	Glu	Ala	Pro	Leu	His	Gln	Leu	Ala	Ser	Asn	Ala	Gly	Val	Glu	Gly	450	455	460	
Ser	Val	Ile	Val	Glu	Lys	Val	Lys	Glu	Ala	Thr	Gly	Asn	Gln	Gly	Tyr	465	470	475	480
Asn	Val	Ile	Thr	Gly	Lys	Ile	Glu	Asp	Leu	Ile	Ala	Ala	Gly	Ile	Ile	485	490	495	
Asp	Pro	Ala	Lys	Val	Val	Arg	Ser	Ala	Leu	Gln	Asn	Ala	Ala	Ser	Ile	500	505	510	
Ala	Gly	Met	Val	Leu	Thr	Thr	Glu	Ala	Leu	Val	Val	Glu	Lys	Pro	Glu	515	520	525	
Pro	Ala	Ala	Pro	Ala	Met	Pro	Asp	Met	Gly	Gly	Met	Gly	Gly	Met	Gly	530	535	540	
Gly	Met	Gly	Gly	Met	Gly	Met	Met									545	550		

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Ala	Lys	Thr	Ile	Ala	Phe	Asp	Lys	Lys	Ala	Arg	Arg	Gly	Leu	Glu	
1				5					10					15		
Arg	Gly	Leu	Asn	Ala	Leu	Ala	Asp	Ala	Val	Lys	Val	Thr	Leu	Gly	Pro	
			20					25					30			
Lys	Gly	Arg	Asn	Val	Val	Leu	Glu	Lys	Lys	Trp	Gly	Ala	Pro	Thr	Ile	
		35					40					45				
Thr	Asn	Asp	Gly	Val	Ser	Ile	Ala	Lys	Glu	Ile	Glu	Leu	Glu	Asp	Pro	
	50					55					60					
Tyr	Glu	Lys	Ile	Gly	Ala	Glu	Leu	Val	Lys	Glu	Val	Ala	Lys	Lys	Thr	
65					70					75					80	
Asp	Asp	Val	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	Gln	
				85					90					95		
Ala	Leu	Val	Arg	Glu	Gly	Leu	Arg	Asn	Val	Ala	Ala	Gly	Ala	Asn	Pro	
			100					105					110			
Leu	Gly	Leu	Lys	Arg	Gly	Ile	Glu	Lys	Ala	Val	Glu	Ala	Val	Thr	Glu	
		115					120					125				
His	Leu	Leu	Lys	Ala	Ala	Lys	Glu	Val	Glu	Thr	Lys	Asp	Gln	Ile	Ala	
	130					135					140					
Ala	Thr	Ala	Gly	Ile	Ser	Ala	Gly	Asp	Pro	Ala	Ile	Gly	Glu	Leu	Ile	
145					150					155					160	
Ala	Glu	Ala	Met	Asp	Lys	Val	Gly	Lys	Glu	Gly	Val	Ile	Thr	Val	Glu	
				165					170					175		
Glu	Ser	Asn	Thr	Phe	Gly	Leu	Gln	Leu	Glu	Leu	Thr	Glu	Gly	Met	Arg	
			180					185						190		
Phe	Asp	Lys	Gly	Phe	Ile	Ser	Gly	Tyr	Phe	Ala	Thr	Asp	Ala	Glu	Arg	
		195					200					205				
Gln	Glu	Ala	Val	Leu	Glu	Asp	Pro	Tyr	Val	Leu	Leu	Val	Ser	Gly	Lys	
	210					215					220					
Ile	Ser	Thr	Val	Lys	Asp	Leu	Leu	Pro	Leu	Leu	Glu	Lys	Val	Ile	Gln	
225					230					235					240	
Ser	Gly	Lys	Pro	Leu	Ala	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	Glu	Ala	
				245					250					255		
Leu	Val	Thr	Leu	Ile	Val	Asn	Lys	Ile	Arg	Gly	Thr	Phe	Lys	Ser	Val	
			260					265					270			
Ala	Ile	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Met	Leu	Gln	
		275					280					285				
Asp	Met	Ala	Ile	Leu	Thr	Gly	Gly	Gln	Val	Ile	Ser	Glu	Glu	Ile	Gly	
	290					295					300					

Leu	Ser	Leu	Asp	Thr	Ala	Gly	Leu	Glu	Val	Leu	Gly	Gln	Ala	Arg	Gln	305	310	315	320
Val	Val	Val	Thr	Lys	Asp	Glu	Thr	Thr	Ile	Val	Asp	Gly	Ala	Gly	Ser	325	330	335	
Lys	Glu	Gln	Ile	Ala	Gly	Arg	Val	Ser	Gln	Ile	Arg	Ala	Glu	Ile	Glu	340	345	350	
Asn	Ser	Asp	Ser	Asp	Tyr	Asp	Arg	Glu	Lys	Leu	Gln	Glu	Arg	Leu	Ala	355	360	365	
Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Ala	Gly	Ala	Ala	Thr	Glu	370	375	380	
Asp	Leu	Lys	Glu	Arg	Lys	His	Arg	Ile	Glu	Asp	Ala	Val	Arg	Asn	Ala	385	390	395	400
Lys	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Ala	Gly	Gly	Gly	Ser	Ser	Leu	405	410	415	
Ala	Gln	Ser	Gly	Thr	Val	Phe	Asp	Ser	Xaa	Ala	Leu	Glu	Gly	Asp	Glu	420	425	430	
Ala	Thr	Gly	Ala	Asn	Ile	Val	Lys	Val	Ala	Leu	Asp	Ala	Pro	Val	Lys	435	440	445	
Gln	Ile	Ala	Val	Asn	Ala	Gly	Leu	Glu	Pro	Gly	Val	Val	Ala	Glu	Lys	450	455	460	
Val	Arg	Asn	Ser	Pro	Ala	Gly	Thr	Gly	Leu	Asn	Ala	Ala	Thr	Gly	Val	465	470	475	480
Tyr	Glu	Asp	Leu	Leu	Ala	Ala	Gly	Ile	Asn	Asp	Pro	Val	Lys	Val	Thr	485	490	495	
Arg	Ser	Ala	Leu	Gln	Asn	Ala	Ala	Ser	Ile	Ala	Ala	Leu	Phe	Leu	Thr	500	505	510	
Thr	Glu	Ala	Val	Val	Ala	Asp	Lys	Pro	Glu	Lys	Ala	Gly	Ala	Pro	Val	515	520	525	
Asp	Pro	Thr	Gly	Gly	Met	Gly	Gly	Met	Asp	Phe	530	535							

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Val Ser Phe Leu Ser Ser Ser Val Ser Arg Leu Pro Leu Arg Ile  
1 5 10 15  
Ala Gly Arg Arg Ile Pro Gly Arg Phe Ala Val Pro Gln Val Arg Thr  
20 25 30  
Tyr Ala Lys Asp Leu Lys Phe Gly Val Asp Ala Arg Ala Ser Leu Leu  
35 40 45  
Thr Gly Val Asp Thr Leu Ala Arg Ala Val Ser Val Thr Leu Gly Pro  
50 55 60  
Lys Gly Arg Asn Val Leu Ile Asp Gln Pro Phe Gly Ser Pro Lys Ile  
65 70 75 80  
Thr Lys Asp Gly Val Thr Val Ala Arg Ser Val Ser Leu Lys Asp Lys  
85 90 95  
Phe Glu Asn Leu Gly Ala Arg Leu Val Gln Asp Val Ala Ser Lys Thr  
100 105 110  
Asn Glu Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Thr Arg  
115 120 125  
Ala Ile Phe Ser Glu Thr Val Arg Asn Val Ala Ala Gly Cys Asn Pro  
130 135 140  
Met Asp Leu Arg Arg Gly Ile Gln Leu Ala Val Asp Asn Val Val Glu  
145 150 155 160  
Phe Leu Gln Ala Asn Lys Arg Asp Ile Thr Thr Ser Glu Glu Ile Ser  
165 170 175  
Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Thr His Ile Gly Glu Leu  
180 185 190  
Leu Ala Lys Ala Met Glu Arg Val Gly Lys Glu Gly Val Ile Thr Val  
195 200 205  
Lys Glu Gly Arg Thr Ile Ser Asp Glu Leu Glu Val Thr Glu Gly Met  
210 215 220  
Lys Phe Asp Arg Gly Tyr Ile Ser Pro Tyr Phe Ile Thr Asp Val Lys  
225 230 235 240  
Ser Gln Lys Val Glu Phe Glu Asn Pro Leu Ile Leu Leu Ser Glu Lys  
245 250 255  
Lys Val Ser Ala Val Gln Asp Ile Leu Pro Ser Leu Glu Leu Ala Ala  
260 265 270  
Gln Gln Arg Arg Pro Leu Val Ile Ile Ala Glu Asp Val Asp Gly Glu  
275 280 285  
Ala Leu Ala Ala Cys Ile Leu Asn Lys Leu Arg Gly Gln Leu Gln Val  
290 295 300

Val	Ala	Ile	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Asn	Arg	Arg	Asn	Met	Leu	305	310	315	320
Gly	Asp	Leu	Ala	Val	Leu	Thr	Asp	Ser	Ala	Val	Phe	Asn	Asp	Glu	Ile	325	330	335	
Asp	Val	Ser	Ile	Glu	Lys	Ala	Gln	Pro	His	His	Leu	Gly	Ser	Cys	Gly	340	345	350	
Ser	Val	Thr	Val	Thr	Lys	Glu	Asp	Thr	Ile	Ile	Met	Lys	Gly	Ala	Gly	355	360	365	
Asp	His	Val	Lys	Val	Asn	Asp	Arg	Cys	Glu	Gln	Ile	Arg	Gly	Val	Met	370	375	380	
Ala	Asp	Pro	Asn	Leu	Thr	Glu	Ser	Glu	Lys	Glu	Lys	Leu	Gln	Glu	Arg	385	390	395	400
Leu	Ala	Lys	Leu	Ser	Gly	Gly	Ile	Ala	Val	Ile	Lys	Val	Gly	Ala	Ser	405	410	415	
Ser	Glu	Val	Glu	Val	Asn	Glu	Lys	Lys	Asp	Arg	Ile	Val	Asp	Ala	Leu	420	425	430	
Asn	Ala	Val	Lys	Ala	Ala	Val	Ser	Glu	Gly	Val	Leu	Pro	Gly	Ala	Gly	435	440	445	
Thr	Ser	Phe	Val	Lys	Ala	Ser	Leu	Arg	Leu	Gly	Asp	Ile	Pro	Thr	Asn	450	455	460	
Asn	Phe	Asp	Gln	Lys	Leu	Gly	Val	Glu	Ile	Val	Arg	Lys	Ala	Ile	Thr	465	470	475	480
Arg	Pro	Ala	Gln	Thr	Ile	Leu	Glu	Asn	Ala	Gly	Leu	Glu	Gly	Asn	Leu	485	490	495	
Ile	Val	Gly	Lys	Leu	Lys	Glu	Leu	Tyr	Gly	Lys	Glu	Phe	Asn	Ile	Gly	500	505	510	
Tyr	Asp	Ile	Ala	Lys	Asp	Arg	Phe	Val	Asp	Leu	Asn	Glu	Ile	Gly	Val	515	520	525	
Leu	Asp	Pro	Leu	Lys	Val	Val	Arg	Thr	Gly	Leu	Val	Asp	Ala	Ser	Gly	530	535	540	
Val	Ala	Ser	Leu	Met	Gly	Thr	Thr	Glu	Cys	Ala	Ile	Val	Asp	Ala	Pro	545	550	555	560
Glu	Glu	Ser	Lys	Ala	Pro	Ala	Gly	Pro	Pro	Gly	Met	Gly	Gly	Met	Gly	565	570	575	
Gly	Met	Pro	Gly	Met	Met											580			

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 572 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met	Leu	Arg	Ser	Ser	Val	Val	Arg	Ser	Arg	Ala	Thr	Leu	Arg	Pro	Leu	1	5	10	15
Leu	Arg	Arg	Ala	Tyr	Ser	Ser	His	Lys	Glu	Leu	Lys	Phe	Gly	Val	Glu	20	25	30	
Gly	Arg	Ala	Ser	Leu	Leu	Lys	Gly	Val	Glu	Thr	Leu	Ala	Glu	Ala	Val	35	40	45	
Ala	Ala	Thr	Leu	Gly	Pro	Lys	Gly	Arg	Asn	Val	Leu	Ile	Glu	Gln	Pro	50	55	60	
Phe	Gly	Pro	Pro	Lys	Ile	Thr	Lys	Asp	Gly	Val	Thr	Val	Ala	Lys	Ser	65	70	75	80
Ile	Val	Leu	Lys	Asp	Lys	Phe	Glu	Asn	Met	Gly	Ala	Lys	Leu	Leu	Gln	85	90	95	
Glu	Val	Ala	Ser	Lys	Thr	Asn	Glu	Ala	Ala	Gly	Asp	Gly	Thr	Thr	Ser	100	105	110	
Ala	Thr	Val	Leu	Gly	Arg	Ala	Ile	Phe	Thr	Glu	Ser	Val	Lys	Asn	Val	115	120	125	
Ala	Ala	Gly	Cys	Asn	Pro	Met	Asp	Leu	Arg	Arg	Gly	Ser	Gln	Val	Ala	130	135	140	
Val	Glu	Lys	Val	Ile	Glu	Phe	Leu	Ser	Ala	Asn	Lys	Lys	Glu	Ile	Thr	145	150	155	160
Thr	Ser	Glu	Glu	Ile	Ala	Gln	Val	Ala	Thr	Ile	Ser	Ala	Asn	Gly	Asp	165	170	175	
Ser	His	Val	Gly	Lys	Leu	Leu	Ala	Ser	Ala	Met	Glu	Lys	Val	Gly	Lys	180	185	190	
Glu	Gly	Val	Ile	Thr	Ile	Arg	Glu	Gly	Arg	Thr	Leu	Glu	Asp	Glu	Leu	195	200	205	
Glu	Val	Thr	Glu	Gly	Met	Arg	Phe	Asp	Arg	Gly	Phe	Ile	Ser	Pro	Tyr	210	215	220	
Phe	Ile	Thr	Asp	Pro	Lys	Ser	Ser	Lys	Val	Glu	Phe	Glu	Lys	Pro	Leu	225	230	235	240
Leu	Leu	Leu	Ser	Glu	Lys	Lys	Ile	Ser	Ser	Ile	Gln	Asp	Ile	Leu	Pro	245	250	255	

Ala	Leu	Glu	Ile	Ser	Asn	Gln	Ser	Arg	Arg	Pro	Leu	Leu	Ile	Ile	Ala	260	265	270
Glu	Asp	Val	Asp	Gly	Glu	Ala	Leu	Ala	Ala	Cys	Ile	Leu	Asn	Lys	Leu	275	280	285
Arg	Gly	Gln	Val	Lys	Val	Cys	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	290	295	300
Asn	Arg	Lys	Asn	Thr	Ile	Gly	Asp	Ile	Ala	Val	Leu	Thr	Gly	Gly	Thr	305	310	315
Val	Phe	Thr	Glu	Glu	Leu	Asp	Leu	Lys	Pro	Glu	Gln	Cys	Thr	Ile	Glu	325	330	335
Asn	Leu	Gly	Ser	Cys	Asp	Ser	Ile	Thr	Val	Thr	Lys	Glu	Asp	Thr	Val	340	345	350
Ile	Leu	Asn	Gly	Ser	Gly	Pro	Lys	Glu	Ala	Ile	Gln	Glu	Arg	Ile	Glu	355	360	365
Gln	Ile	Lys	Gly	Ser	Ile	Asp	Ile	Thr	Thr	Thr	Asn	Ser	Tyr	Glu	Lys	370	375	380
Glu	Lys	Leu	Gln	Glu	Arg	Leu	Ala	Lys	Leu	Ser	Gly	Gly	Val	Ala	Val	385	390	395
Ile	Arg	Val	Gly	Gly	Ala	Ser	Glu	Val	Glu	Val	Gly	Glu	Lys	Lys	Asp	405	410	415
Arg	Tyr	Asp	Asp	Ala	Leu	Asn	Ala	Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	420	425	430
Ile	Leu	Pro	Gly	Gly	Gly	Thr	Ala	Leu	Val	Lys	Ala	Ser	Arg	Val	Leu	435	440	445
Asp	Glu	Val	Val	Val	Asp	Asn	Phe	Asp	Gln	Lys	Leu	Gly	Val	Asp	Ile	450	455	460
Ile	Arg	Lys	Ala	Ile	Thr	Arg	Pro	Ala	Lys	Gln	Ile	Ile	Glu	Asn	Ala	465	470	475
Gly	Glu	Glu	Gly	Ser	Val	Ile	Ile	Gly	Lys	Leu	Ile	Asp	Glu	Tyr	Gly	485	490	495
Asp	Asp	Phe	Ala	Lys	Gly	Tyr	Asp	Ala	Ser	Lys	Ser	Glu	Tyr	Thr	Asp	500	505	510
Met	Leu	Ala	Thr	Gly	Ile	Ile	Asp	Pro	Phe	Lys	Val	Val	Arg	Ser	Gly	515	520	525
Leu	Val	Asp	Ala	Ser	Gly	Val	Ala	Ser	Leu	Leu	Ala	Thr	Thr	Glu	Val	530	535	540
Ala	Ile	Val	Asp	Ala	Pro	Glu	Pro	Pro	Ala	Ala	Ala	Gly	Ala	Gly	Gly	545	550	555

Met Pro Gly Gly Met Pro Gly Met Pro Gly Met Met  
565 570

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Ile	Ser	Thr	Leu	Arg	Gly	Lys	Ile	Phe	Asn	Asn	Gly	Ser	Asn	Arg	1	5	10	15
Asn	Lys	Cys	Val	Ser	Ile	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Asn	Ile	Ser	20	25	30	
Lys	Asp	Ile	Arg	Phe	Gly	Ser	Asp	Ala	Arg	Thr	Ala	Met	Leu	Thr	Gly	35	40	45	
Cys	Asn	Lys	Leu	Ala	Asp	Ala	Val	Ser	Val	Thr	Leu	Gly	Pro	Lys	Gly	50	55	60	
Arg	Asn	Val	Ile	Ile	Glu	Gln	Ser	Phe	Gly	Ser	Pro	Lys	Ile	Thr	Lys	65	70	75	80
Asp	Gly	Val	Thr	Val	Ala	Lys	Ser	Ile	Glu	Phe	Asn	Asn	Lys	Leu	Ala	85	90	95	
Asn	Leu	Gly	Ala	Gln	Met	Val	Lys	Gln	Val	Ala	Ala	Asn	Thr	Asn	Gly	100	105	110	
Lys	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Ile	Leu	Ala	Arg	Ser	Ile	115	120	125	
Phe	Gln	Gln	Gly	Cys	Lys	Ala	Val	Asp	Ser	Gly	Met	Asn	Pro	Met	Asp	130	135	140	
Leu	Leu	Arg	Gly	Ile	Asn	Lys	Gly	Val	Glu	Lys	Val	Leu	Glu	Tyr	Leu	145	150	155	160
Asn	Ser	Ile	Lys	Lys	Asp	Val	Thr	Thr	Thr	Glu	Glu	Ile	Phe	Asn	Val	165	170	175	
Ala	Ser	Ile	Ser	Asn	Gly	Asp	Lys	Asn	Ile	Gly	Gln	Leu	Ile	Ala	Asp	180	185	190	
Thr	Met	Lys	Lys	Val	Gly	Lys	Glu	Gly	Thr	Ile	Thr	Val	Thr	Glu	Gly	195	200	205	
Lys	Thr	Leu	Gln	His	Glu	Leu	Glu	Ile	Val	Glu	Gly	Ile	Lys	Phe	Asp	210	215	220	



Arg	Gly	Tyr	Ile	Ser	Pro	Tyr	Phe	Ile	Asn	Asn	Ser	Gln	Lys	Val	Glu	225	230	235	240
Leu	Asp	Lys	Pro	Tyr	Ile	Leu	Ile	His	Glu	Lys	Lys	Ile	Ser	Thr	Val	245	250		255
Lys	Ser	Leu	Leu	Pro	Val	Leu	Glu	His	Val	Leu	Gln	Asn	Gln	Ser	Ser	260	265		270
Leu	Leu	Val	Ile	Ala	Glu	Asp	Val	Asp	Ser	Asp	Ala	Leu	Ala	Thr	Leu	275	280		285
Ile	Val	Asn	Lys	Leu	Arg	Leu	Gly	Leu	Lys	Ile	Cys	Ala	Val	Lys	Ala	290	295	300	
Pro	Gly	Phe	Gly	Glu	His	Arg	Lys	Ala	Leu	Ile	His	Asp	Ile	Ala	Val	305	310	315	320
Met	Thr	Gly	Ala	Lys	Val	Ile	Thr	Glu	Glu	Thr	Gly	Leu	Lys	Leu	Asp	325	330		335
Asp	Pro	Gln	Val	Val	Ser	Tyr	Leu	Gly	Lys	Ala	Lys	Ser	Ile	Asn	Val	340	345		350
Thr	Lys	Asp	Ser	Thr	Leu	Ile	Met	Glu	Gly	Glu	Gly	Lys	Lys	Glu	Glu	355	360	365	
Ile	Asn	Glu	Arg	Cys	Glu	Ser	Ile	Arg	Asn	Ala	Ile	Lys	Met	Asn	Thr	370	375	380	
Ser	Asp	Tyr	Glu	Lys	Glu	Lys	Leu	Gln	Glu	Arg	Leu	Ala	Lys	Ile	Thr	385	390	395	400
Gly	Gly	Val	Ala	Leu	Ile	Lys	Val	Gly	Gly	Ile	Ser	Glu	Val	Glu	Val	405	410		415
Asn	Glu	Ile	Lys	Asp	Arg	Ile	Gln	Asp	Ala	Leu	Cys	Ala	Thr	Lys	Ala	420	425		430
Ala	Val	Glu	Glu	Gly	Ile	Val	Pro	Gly	Gly	Gly	Ser	Ala	Leu	Leu	Phe	435	440		445
Ala	Ser	Lys	Glu	Leu	Asp	Ser	Val	Gln	Thr	Asp	Asn	Tyr	Asp	Gln	Arg	450	455	460	
Val	Gly	Val	Asn	Ile	Ile	Lys	Asp	Ala	Cys	Lys	Ala	Pro	Ile	Lys	Gln	465	470	475	480
Ile	Ala	Glu	Asn	Ala	Gly	His	Glu	Gly	Ser	Val	Val	Ala	Gly	Asn	Ile	485	490		495
Leu	Lys	Asp	Lys	Asn	Ser	Asn	Ile	Gly	Phe	Asn	Ala	Gln	Glu	Gly	Lys	500	505		510
Tyr	Val	Asp	Met	Ile	Glu	Ser	Gly	Ile	Ile	Asp	Pro	Thr	Lys	Val	Val	515	520	525	

Lys Thr Ala Ile Ser Asp Ala Ala Ser Ile Ala Ser Leu Met Thr Thr  
 530 535 540  
 Thr Glu Val Ala Ile Val Asp Phe Lys Asp Ser Lys Asn Glu Glu Ser  
 545 550 555 560  
 Ser Gln His Met Asn Ser Val Asn Ser Met Gly Asp Met Gly Gly Met  
 565 570 575  
 Tyr

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Thr Asn Val Val Val Ser Gly Glu Gln Leu Gln Gln Ala Phe Arg  
 1 5 10 15  
 Glu Val Ala Ala Val Ile Asp Ser Thr Val Ala Val Thr Ala Gly Pro  
 20 25 30  
 Arg Gly Lys Thr Val Gly Ile Asn Lys Pro Tyr Gly Ala Pro Glu Ile  
 35 40 45  
 Thr Lys Asp Gly Tyr Lys Val Met Lys Gly Ile Lys Pro Glu Lys Pro  
 50 55 60  
 Leu Asn Ala Ala Ile Thr Ser Ile Phe Ala Gln Ser Cys Ser Gln Cys  
 65 70 75 80  
 Asn Asp Lys Val Gly Asp Gly Thr Thr Thr Cys Ser Ile Leu Thr Ser  
 85 90 95  
 Gly Met Ile Val Glu Ala Ser Lys Ser Ile Ala Ala Gly Asn Asp Arg  
 100 105 110  
 Ile Ser Ile Lys Asn Gly Met Gln Lys Ala Lys Asp Val Val Leu Lys  
 115 120 125  
 Glu Val Ala Ser Met Ala Arg Thr Ile Ser Leu Glu Lys Ile Asp Glu  
 130 135 140  
 Val Ala Gln Val Ala Ile Ile Ser Ala Asn Gly Asp Arg Ser Ile Gly  
 145 150 155 160  
 Ser Asn Ile Ala Asp Ala Val Lys Lys Val Gly Lys Glu Gly Val Ile  
 165 170 175

Thr	Val	Glu	Glu	Ser	Lys	Gly	Ser	Lys	Glu	Leu	Glu	Val	Glu	Leu	Thr	180	185	190	
Thr	Gly	Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro	Tyr	Phe	Ile	Thr	195	200	205	
Asn	Asn	Glu	Lys	Met	Ile	Val	Glu	Leu	Asp	Asp	Pro	Tyr	Leu	Leu	Ile	210	215	220	
Thr	Glu	Lys	Lys	Leu	Asn	Ile	Ile	Gln	Pro	Leu	Leu	Ser	Ile	Leu	Glu	225	230	235	240
Ala	Val	Val	Lys	Ser	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Ile	245	250	255	
Glu	Gly	Glu	Ala	Leu	Ser	Thr	Leu	Val	Ile	Asn	Lys	Leu	Arg	Gly	Gly	260	265	270	
Leu	Lys	Val	Ala	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	275	280	285	
Glu	Met	Leu	Glu	Asp	Ile	Ala	Ala	Leu	Thr	Asn	Ala	Lys	Tyr	Val	Ile	290	295	300	
Lys	Asp	Glu	Leu	Gly	Ile	Lys	Met	Glu	Asp	Leu	Thr	Leu	Glu	Asp	Leu	305	310	315	320
Gly	Ile	Ala	Lys	Asn	Val	Lys	Ile	Thr	Lys	Asp	Asn	Thr	Thr	Ile	Val	325	330	335	
Ser	Glu	Asn	Arg	Val	Thr	Asp	Arg	Val	Lys	Ala	Arg	Ile	Glu	Gln	Ile	340	345	350	
Lys	Ser	Gln	Ile	Glu	Ser	Ser	Thr	Ser	Asp	Tyr	Asp	Lys	Glu	Lys	Leu	355	360	365	
Arg	Glu	Arg	Leu	Ala	Lys	Leu	Ser	Gly	Gly	Val	Ala	Val	Leu	Lys	Val	370	375	380	
Gly	Gly	Ala	Thr	Glu	Leu	Glu	Val	Lys	Glu	Arg	Arg	Asp	Arg	Val	Glu	385	390	395	400
Asp	Gln	Leu	His	Ala	Thr	Arg	Ala	Ala	Ile	Glu	Glu	Gly	Ile	Val	Pro	405	410	415	
Gly	Gly	Gly	Val	Ala	Leu	Leu	Tyr	Ala	Ser	Ser	Ala	Leu	Asp	Lys	Leu	420	425	430	
Lys	Gly	Ala	Asp	Asp	Glu	Glu	Gln	Ile	Gly	Ile	Asn	Ile	Ile	Lys	Lys	435	440	445	
Val	Leu	Ser	Val	Pro	Ile	Lys	Arg	Leu	Val	Lys	Asn	Ala	Gly	Leu	Glu	450	455	460	
Ser	Ala	Val	Ile	Ile	Asp	Tyr	Leu	Ile	Lys	Gln	Asn	Asn	Lys	Glu	Leu	465	470	475	480

Ile	Tyr	Asn	Val	Glu	Ala	Met	Ser	Tyr	Ala	Asn	Ala	Phe	Ala	Ala	Gly
				485					490					495	
Val	Ile	Asp	Pro	Ala	Lys	Val	Val	Arg	Ile	Ala	Phe	Glu	Thr	Ala	Ile
			500					505					510		
Ser	Val	Ala	Ser	Val	Leu	Ile	Thr	Thr	Glu	Ser	Met	Ile	Val	Asp	Ile
		515					520					525			
Pro	Asn	Lys	Asp	Glu	Asn	Ala	Ser	Ser	Pro	Met	Gly	Ala	Gly	Gly	Met
	530					535					540				
Gly	Arg	Met	Asn	Asp	Phe										
545					550										

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Leu	Arg	Leu	Ala	Arg	Lys	Gly	Leu	Gln	Thr	Ala	Val	Val	Arg	Ser
1				5					10					15	
Tyr	Ala	Lys	Asp	Val	Lys	Phe	Gly	Ala	Glu	Gly	Arg	Gln	Ala	Met	Leu
		20					25						30		
Val	Gly	Val	Asn	Leu	Leu	Ala	Asp	Ala	Val	Ser	Val	Thr	Met	Gly	Pro
		35					40					45			
Lys	Gly	Arg	Asn	Val	Ile	Ile	Glu	Gln	Ser	Trp	Gly	Ser	Pro	Lys	Ile
	50					55					60				
Thr	Lys	Asp	Gly	Val	Thr	Val	Ala	Lys	Ser	Ile	Asp	Leu	Lys	Asp	Lys
65					70					75				80	
Tyr	Gln	Asn	Leu	Gly	Ala	Lys	Leu	Ile	Gln	Asp	Val	Ala	Asn	Lys	Ala
				85					90					95	
Asn	Glu	Glu	Ala	Gly	Asp	Gly	Thr	Thr	Cys	Ala	Thr	Val	Leu	Thr	Arg
			100					105					110		
Ala	Ile	Ala	Lys	Glu	Gly	Phe	Glu	Arg	His	Ser	Ser	Arg	Gly	Asn	Ala
		115					120					125			
Val	Glu	Ile	Arg	Arg	Gly	Val	Met	Asn	Ala	Val	Glu	Val	Val	Val	Ala
	130					135					140				
Glu	Leu	Lys	Lys	Ile	Ser	Lys	Lys	Val	Thr	Thr	Pro	Glu	Glu	Ile	Ala
145					150					155					160

Gln	Val	Ala	Thr	Ile	Ser	Ala	Asn	Gly	Asp	Thr	Val	Val	Gly	Asn	Leu	165	170	175
Ile	Ser	Asp	Ala	Met	Lys	Lys	Val	Gly	Thr	Thr	Gly	Val	Ile	Thr	Val	180	185	190
Lys	Asp	Gly	Lys	Thr	Leu	Asn	Asp	Gln	Leu	Glu	Leu	Ile	Glu	Gly	Met	195	200	205
Lys	Phe	Asp	Arg	Gly	Tyr	Ile	Ser	Pro	Tyr	Phe	Ile	Thr	Ser	Ala	Lys	210	215	220
Gly	Ala	Lys	Val	Glu	Tyr	Glu	Lys	Ala	Leu	Val	Leu	Leu	Ser	Glu	Lys	225	230	235
Lys	Ile	Ser	Gln	Val	Gln	Asp	Ile	Val	Pro	Ala	Leu	Glu	Leu	Ala	Asn	245	250	255
Lys	Leu	Arg	Arg	Pro	Leu	Val	Ile	Ile	Ala	Glu	Asp	Val	Asp	Gly	Glu	260	265	270
Ala	Leu	Thr	Thr	Leu	Val	Leu	Asn	Arg	Leu	Lys	Val	Gly	Leu	Gln	Val	275	280	285
Val	Ala	Ile	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Asn	Arg	Lys	Asn	Ala	Leu	290	295	300
Lys	Asp	Met	Gly	Ile	Ala	Thr	Gly	Ala	Ser	Ile	Phe	Gly	Asp	Glu	Thr	305	310	315
Leu	Asp	Leu	Arg	Leu	Glu	Asp	Ile	Thr	Ala	Asn	Asp	Leu	Gly	Glu	Val	325	330	335
Asp	Glu	Val	Thr	Ile	Thr	Lys	Asp	Asp	Thr	Leu	Leu	Leu	Arg	Gly	Arg	340	345	350
Gly	Asp	Gln	Thr	Glu	Ile	Glu	Lys	Arg	Ile	Glu	Glu	Ile	Thr	Asp	Glu	355	360	365
Ile	Glu	Arg	Ser	Thr	Ser	Asp	Tyr	Glu	Lys	Glu	Lys	Leu	Asn	Glu	Arg	370	375	380
Leu	Ala	Lys	Leu	Ser	Lys	Gly	Val	Ala	Val	Leu	Lys	Ile	Gly	Gly	Gly	385	390	395
Ser	Glu	Val	Glu	Val	Gly	Glu	Lys	Lys	Asp	Arg	Val	Thr	Asp	Ala	Leu	405	410	415
Cys	Ala	Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Pro	Gly	Gly	Gly	420	425	430
Val	Ala	Leu	Leu	Arg	Ser	Leu	Thr	Ala	Leu	Lys	Asn	Tyr	Lys	Ala	Ala	435	440	445
Asn	Glu	Asp	Gln	Gln	Ile	Gly	Val	Asn	Ile	Val	Lys	Lys	Ala	Leu	Thr	450	455	460

Gln	Pro	Ile	Ala	Thr	Ile	Val	Lys	Asn	Ala	Gly	Leu	Glu	Pro	Ser	Ser	465	470	475	480
Ile	Ile	Asp	Glu	Val	Thr	Gly	Asn	Ser	Asn	Thr	Ser	Tyr	Gly	Tyr	Asp	485	490	495	
Ala	Leu	Asn	Gly	Lys	Phe	Val	Asp	Met	Phe	Glu	Ala	Gly	Ile	Ile	Asp	500	505	510	
Pro	Thr	Lys	Val	Val	Arg	Thr	Ala	Leu	Gln	Asp	Ala	Ser	Gly	Val	Ala	515	520	525	
Ser	Leu	Leu	Ala	Thr	Thr	Glu	Cys	Val	Val	Thr	Glu	Ile	Pro	Lys	Glu	530	535	540	
Glu	Ala	Val	Gly	Gly	Pro	Ala	Gly	Gly	Met	Gly	Gly	Met	Gly	Gly	Met	545	550	555	560
Gly	Gly	Met	Gly	Gly	Met	Gly	Phe									565			

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Phe	Arg	Leu	Pro	Val	Ser	Leu	Ala	Arg	Ser	Ser	Ile	Ser	Arg	Gln	1	5	10	15
Leu	Ala	Met	Arg	Gly	Tyr	Ala	Lys	Asp	Val	Arg	Phe	Gly	Pro	Glu	Val	20	25	30	
Arg	Ala	Met	Met	Leu	Gln	Gly	Val	Asp	Val	Leu	Ala	Asp	Ala	Val	Ala	35	40	45	
Val	Thr	Met	Gly	Pro	Lys	Gly	Arg	Asn	Val	Ile	Ile	Glu	Gln	Ser	Val	50	55	60	
Gly	Leu	Ala	Lys	Ile	Thr	Lys	Asp	Gly	Val	Thr	Val	Ala	Lys	Ser	Ile	65	70	75	80
Glu	Leu	Lys	Asp	Lys	Phe	Gln	Asn	Ile	Gly	Ala	Lys	Leu	Val	Gln	Asp	85	90	95	
Leu	Ala	Asn	Asn	Thr	Asn	Glu	Glu	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	100	105	110	
Thr	Phe	Leu	Ala	Arg	Ala	Ile	Ala	Lys	Glu	Gly	Phe	Glu	Lys	Ile	Ser	115	120	125	

Lys	Gly	Gly	Asn	Pro	Val	Glu	Ile	Arg	Arg	Gly	Val	Met	Leu	Ala	Val	130	135	140	
Glu	Thr	Val	Lys	Asp	Asn	Leu	Lys	Thr	Met	Ser	Arg	Pro	Val	Ser	Thr	145	150	155	160
Pro	Glu	Glu	Ile	Ala	Gln	Val	Ala	Thr	Ile	Ser	Ala	Asn	Gly	Asp	Arg	165	170	175	
Glu	Ile	Gly	Asn	Gly	Lys	Val	Ser	Val	Ser	Glu	Ala	Met	Lys	Lys	Val	180	185	190	
Gly	Arg	Asp	Gly	Val	Ile	Thr	Val	Lys	Asp	Gly	Lys	Thr	Leu	Thr	Asp	195	200	205	
Glu	Leu	Glu	Val	Ile	Glu	Gly	Thr	Met	Arg	Phe	Asp	Arg	Gly	Tyr	Ile	210	215	220	
Ser	Pro	Tyr	Phe	Ile	Asn	Ser	Ser	Lys	Gly	Ala	Lys	Val	Glu	Phe	Gln	225	230	235	240
Asp	Ala	Leu	Leu	Leu	Leu	Ser	Glu	Lys	Lys	Ile	Ser	Ser	Val	Ala	Glu	245	250	255	
His	His	Ser	Pro	Leu	Trp	Arg	Leu	Ala	Ser	Arg	Arg	Thr	Arg	Lys	Pro	260	265	270	
Leu	Val	Ile	Ile	Ala	Glu	Asp	Ile	Asp	Gly	Glu	Ala	Leu	Ser	Thr	Leu	275	280	285	
Val	Val	Asn	Arg	Leu	Lys	Ile	Gly	Leu	Gln	Val	Ala	Ala	Val	Lys	Ala	290	295	300	
Pro	Gly	Phe	Gly	Asp	Asn	Arg	Lys	Ser	Thr	Leu	Thr	Asp	Met	Ala	Thr	305	310	315	320
Ser	Gly	Gly	Ile	Val	Phe	Gly	Asp	Asp	Val	Ser	Leu	Val	Lys	Leu	Glu	325	330	335	
Asp	Val	Lys	Val	Ser	Asp	Leu	Gly	Gln	Val	Gly	Glu	Val	Val	Ile	Thr	340	345	350	
Lys	Asp	Asp	Thr	Leu	Leu	Leu	Lys	Gly	Lys	Gly	Lys	Lys	Asp	Asp	Val	355	360	365	
Leu	Arg	Arg	Ala	Asn	Gln	Ile	Arg	Thr	Lys	Ile	Glu	Asp	Thr	Thr	Ser	370	375	380	
Glu	Tyr	Glu	Lys	Glu	Lys	Leu	Gln	Glu	Arg	Leu	Ala	Arg	Leu	Ala	Ser	385	390	395	400
Gly	Val	Ala	Leu	Arg	Val	Gly	Gly	Ser	Ser	Glu	Val	Glu	Val	Asn	Glu	405	410	415	
Lys	Lys	Asp	Arg	Val	His	Asp	Ala	Leu	Asn	Ala	Thr	Arg	Ala	Ala	Val	420	425	430	

Glu	Glu	Gly	Ile	Val	Pro	Gly	Gly	Gly	Arg	Pro	Leu	Leu	Arg	Cys	Ile			
		435						440				445						
Glu	Lys	Leu	Glu	Gly	Val	Glu	Thr	Thr	Asn	Glu	Asp	Gln	Lys	Leu	Gly			
		450						455				460						
Val	Glu	Ile	Val	Arg	Arg	Ala	Leu	Arg	Met	Pro	Cys	Met	Thr	Ile	Ala			
					470					475					480			
Lys	Asn	Ala	Gly	Val	Asp	Gly	Ala	Met	Val	Val	Ala	Lys	Val	Glu	Asn			
				485					490						495			
Gln	Ala	Gly	Asp	Tyr	Gly	Tyr	Asp	Ala	Lys	Gly	Glu	Tyr	Gly	Asn	Leu			
			500					505						510				
Ile	Glu	Lys	Gly	Ile	Ile	Asp	Pro	Thr	Lys	Val	Val	Arg	Thr	Ala	Ile			
		515					520						525					
Thr	Asp	Ala	Ser	Gly	Val	Ala	Ser	Leu	Leu	Thr	Thr	Ala	Glu	Ala	Val			
		530				535						540						
Val	Thr	Glu	Ile	Pro	Lys	Glu	Asp	Gly	Ala	Pro	Ala	Met	Pro	Gly	Met			
					550					555					560			
Gly	Gly	Met	Gly	Gly	Met	Gly	Gly	Met	Gly	Gly	Met	Gly	Gly	Met	Met			
				565					570						575			

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Leu	Arg	Leu	Pro	Thr	Val	Phe	Arg	Gln	Met	Arg	Pro	Val	Ser	Arg			
1				5					10					15				
Val	Leu	Ala	Pro	His	Leu	Thr	Arg	Ala	Tyr	Ala	Lys	Asp	Val	Lys	Phe			
			20					25					30					
Gly	Ala	Asp	Ala	Arg	Ala	Leu	Met	Leu	Gln	Gly	Val	Asp	Leu	Leu	Ala			
		35					40					45						
Asp	Ala	Val	Ala	Val	Thr	Met	Gly	Pro	Lys	Gly	Arg	Thr	Val	Ile	Ile			
		50				55					60							
Glu	Gln	Gly	Trp	Gly	Ser	Pro	Lys	Val	Thr	Lys	Asp	Gly	Val	Thr	Val			
		65			70					75					80			
Ala	Lys	Ser	Ile	Asp	Leu	Lys	Asp	Lys	Tyr	Lys	Asn	Ile	Gly	Ala	Lys			



85								90				95						
Leu	Val	Gln	Asp	Val	Ala	Asn	Asn	Thr	Asn	Glu	Glu	Ala	Gly	Asp	Gly			
			100					105					110					
Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	Arg	Ser	Ile	Ala	Lys	Glu	Gly	Phe			
		115					120					125						
Glu	Lys	Ile	Ser	Lys	Gly	Ala	Asn	Pro	Val	Glu	Ile	Arg	Arg	Gly	Val			
	130					135					140							
Met	Leu	Ala	Val	Asp	Ala	Val	Ile	Ala	Glu	Leu	Lys	Lys	Gln	Ser	Lys			
145					150					155					160			
Pro	Val	Thr	Thr	Pro	Glu	Glu	Ile	Ala	Gln	Val	Ala	Thr	Ile	Ser	Ala			
				165					170					175				
Asn	Gly	Asp	Lys	Glu	Ile	Gly	Asn	Ile	Ile	Ser	Asp	Ala	Met	Lys	Lys			
			180					185					190					
Val	Gly	Arg	Lys	Gly	Val	Ile	Thr	Val	Lys	Asp	Gly	Lys	Thr	Leu	Asn			
		195					200					205						
Asp	Glu	Leu	Glu	Ile	Ile	Glu	Gly	Met	Lys	Phe	Asp	Arg	Gly	Tyr	Ile			
	210					215					220							
Ser	Pro	Tyr	Phe	Ile	Asn	Thr	Ser	Lys	Gly	Gln	Lys	Cys	Glu	Phe	Gln			
225					230					235					240			
Asp	Ala	Tyr	Val	Leu	Leu	Ser	Glu	Lys	Lys	Ile	Ser	Ser	Ile	Gln	Ser			
				245					250					255				
Ile	Val	Pro	Ala	Leu	Glu	Ile	Ala	Asn	Ala	His	Arg	Lys	Pro	Leu	Val			
			260					265					270					
Ile	Ile	Ala	Glu	Asp	Val	Asp	Gly	Glu	Ala	Leu	Ser	Thr	Leu	Val	Leu			
		275					280					285						
Asn	Arg	Leu	Lys	Val	Gly	Leu	Gln	Val	Val	Ala	Val	Lys	Ala	Pro	Gly			
		290				295					300							
Phe	Gly	Asp	Asn	Arg	Lys	Asn	Gln	Leu	Lys	Asp	Met	Ala	Ile	Ala	Thr			
305					310					315					320			
Gly	Gly	Ala	Val	Phe	Gly	Glu	Glu	Gly	Leu	Thr	Leu	Asn	Leu	Glu	Asp			
				325				330					335					
Val	Gln	Pro	His	Asp	Leu	Gly	Lys	Val	Gly	Glu	Val	Ile	Val	Thr	Lys			
			340					345					350					
Asp	Asp	Ala	Met	Leu	Leu	Lys	Gly	Lys	Gly	Asp	Lys	Ala	Gln	Ile	Glu			
		355					360					365						
Lys	Arg	Ile	Gln	Glu	Ile	Ile	Glu	Gln	Leu	Asp	Val	Thr	Thr	Ser	Glu			
		370				375					380							
Tyr	Glu	Lys	Glu	Lys	Leu	Asn	Glu	Arg	Leu	Ala	Lys	Leu	Ser	Asp	Gly			
385					390					395					400			

Val	Ala	Val	Leu	Lys	Val	Gly	Gly	Thr	Ser	Asp	Val	Glu	Val	Asn	Glu			
				405					410					415				
Lys	Lys	Asp	Arg	Val	Thr	Asp	Ala	Leu	Asn	Ala	Thr	Arg	Ala	Ala	Val			
			420					425					430					
Glu	Glu	Gly	Ile	Val	Leu	Gly	Gly	Gly	Cys	Ala	Leu	Leu	Arg	Cys	Ile			
		435					440					445						
Pro	Ala	Leu	Asp	Ser	Leu	Thr	Pro	Ala	Asn	Glu	Asp	Gln	Lys	Ile	Gly			
	450					455					460							
Ile	Glu	Ile	Ile	Lys	Arg	Thr	Leu	Lys	Ile	Pro	Ala	Met	Thr	Ile	Ala			
465				470					475						480			
Lys	Asn	Ala	Gly	Val	Glu	Gly	Ser	Leu	Ile	Val	Glu	Lys	Ile	Met	Gln			
			485					490					495					
Ser	Ser	Ser	Glu	Val	Gly	Tyr	Asp	Ala	Met	Ala	Gly	Asp	Phe	Val	Asn			
			500				505						510					
Met	Val	Glu	Lys	Gly	Ile	Ile	Asp	Pro	Thr	Lys	Val	Val	Arg	Thr	Ala			
	515					520						525						
Leu	Leu	Asp	Ala	Ala	Gly	Val	Ala	Ser	Leu	Leu	Thr	Thr	Ala	Glu	Val			
	530					535					540							
Val	Val	Thr	Glu	Ile	Pro	Lys	Glu	Glu	Lys	Asp	Pro	Gly	Met	Gly	Ala			
545				550					555					560				
Met	Gly	Gly	Met	Gly	Gly	Gly	Met	Gly	Gly	Gly	Met	Phe						
			565				570											

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met	Tyr	Arg	Phe	Ala	Ser	Asn	Leu	Ala	Ser	Lys	Ala	Arg	Ile	Ala	Gln			
1				5					10				15					
Asn	Ala	Arg	Gln	Val	Ser	Ser	Arg	Met	Ser	Trp	Ser	Arg	Asn	Tyr	Ala			
			20				25						30					
Ala	Lys	Glu	Ile	Lys	Phe	Gly	Val	Glu	Ala	Arg	Ala	Leu	Met	Leu	Lys			
	35					40					45							
Gly	Val	Glu	Asp	Leu	Ala	Asp	Ala	Val	Lys	Val	Thr	Met	Gly	Pro	Lys			

50							55									60
Gly	Arg	Asn	Val	Val	Ile	Glu	Gln	Ser	Trp	Gly	Ala	Pro	Lys	Val	Thr	
65					70					75					80	
Lys	Asp	Gly	Val	Thr	Val	Ala	Lys	Ser	Ile	Glu	Phe	Lys	Asp	Lys	Ile	
				85					90					95		
Lys	Asn	Val	Gly	Ala	Ser	Leu	Val	Lys	Gln	Val	Ala	Asn	Ala	Thr	Asn	
			100					105					110			
Asp	Val	Ala	Gly	Asp	Gly	Thr	Thr	Cys	Ala	Thr	Val	Leu	Thr	Arg	Ala	
		115					120					125				
Ile	Phe	Ala	Glu	Gly	Cys	Lys	Ser	Val	Ala	Ala	Gly	Met	Asn	Ala	Met	
	130					135					140					
Asp	Leu	Arg	Arg	Gly	Ile	Ser	Met	Ala	Val	Asp	Ala	Val	Val	Thr	Asn	
145					150					155					160	
Leu	Lys	Ser	Lys	Ala	Arg	Met	Ile	Ser	Thr	Ser	Glu	Glu	Ile	Ala	Gln	
				165					170					175		
Val	Gly	Thr	Ile	Ser	Ala	Asn	Gly	Glu	Arg	Glu	Ile	Gly	Glu	Leu	Ile	
			180					185					190			
Ala	Lys	Ala	Met	Glu	Lys	Val	Gly	Lys	Glu	Gly	Val	Ile	Thr	Ile	Gln	
		195					200					205				
Asp	Gly	Lys	Thr	Leu	Phe	Asn	Glu	Leu	Glu	Val	Val	Glu	Gly	Met	Lys	
	210					215					220					
Leu	Asp	Arg	Gly	Tyr	Thr	Ser	Pro	Tyr	Phe	Ile	Thr	Asn	Gln	Lys	Thr	
225					230					235					240	
Gln	Lys	Cys	Glu	Leu	Asp	Asp	Pro	Leu	Ile	Leu	Ile	His	Glu	Lys	Lys	
				245					250					255		
Ile	Ser	Ser	Ile	Asn	Ser	Ile	Val	Lys	Val	Leu	Glu	Leu	Ala	Leu	Lys	
			260					265					270			
Arg	Gln	Arg	Pro	Leu	Leu	Ile	Val	Ser	Glu	Asp	Val	Glu	Ser	Asp	Ala	
		275					280					285				
Leu	Ala	Thr	Leu	Ile	Leu	Asn	Lys	Leu	Arg	Ala	Gly	Ile	Lys	Val	Cys	
	290					295					300					
Ala	Ile	Lys	Ala	Pro	Gly	Phe	Gly	Glu	Asn	Arg	Lys	Ala	Asn	Leu	Gln	
305					310					315					320	
Asp	Leu	Ala	Ala	Leu	Thr	Gly	Gly	Glu	Val	Ile	Thr	Asp	Glu	Leu	Gly	
				325					330					335		
Met	Asn	Leu	Glu	Lys	Val	Asp	Leu	Ser	Met	Leu	Gly	Thr	Cys	Lys	Lys	
			340					345					350			
Val	Thr	Val	Ser	Lys	Asp	Asp	Thr	Val	Ile	Leu	Asp	Gly	Ala	Gly	Asp	
		355					360					365				



1		5		10		15											
Ser	Ser	Ser	Ala	Ala	Arg	Gln	Val	Gly	Ser	Arg	Leu	Ala	Trp	Ser	Arg		
			20					25					30				
Asn	Tyr	Ala	Ala	Lys	Asp	Ile	Lys	Phe	Gly	Val	Glu	Ala	Arg	Ala	Leu		
		35					40					45					
Met	Leu	Arg	Gly	Val	Glu	Glu	Leu	Ala	Asp	Ala	Val	Lys	Val	Thr	Met		
	50					55					60						
Gly	Pro	Lys	Gly	Arg	Asn	Val	Val	Ile	Glu	Gln	Ser	Phe	Gly	Ala	Pro		
65					70					75					80		
Lys	Val	Thr	Lys	Asp	Gly	Val	Thr	Val	Ala	Lys	Ser	Ile	Glu	Phe	Lys		
				85					90					95			
Asp	Arg	Val	Lys	Asn	Val	Gly	Ala	Ser	Leu	Val	Lys	Gln	Val	Ala	Asn		
			100					105					110				
Ala	Thr	Asn	Asp	Asn	Ala	Gly	Asp	Gly	Thr	Thr	Cys	Ala	Thr	Val	Leu		
		115					120					125					
Thr	Lys	Ala	Ile	Phe	Thr	Glu	Gly	Cys	Lys	Ser	Val	Ala	Ala	Gly	Met		
	130					135					140						
Asn	Ala	Met	Asp	Leu	Arg	Arg	Gly	Ile	Ser	Met	Ala	Val	Asp	Ala	Val		
145					150					155					160		
Val	Thr	Asn	Leu	Lys	Gly	Met	Ala	Arg	Met	Ile	Ser	Thr	Ser	Glu	Glu		
			165						170					175			
Ile	Ala	Gln	Val	Gly	Thr	Ile	Ser	Ala	Asn	Gly	Glu	Arg	Glu	Ile	Gly		
		180						185					190				
Glu	Leu	Ile	Ala	Lys	Ala	Met	Glu	Lys	Val	Gly	Lys	Glu	Gly	Val	Ile		
	195						200					205					
Thr	Ile	Ala	Asp	Gly	Asn	Thr	Leu	Tyr	Asn	Glu	Leu	Glu	Val	Val	Glu		
	210					215					220						
Gly	Met	Lys	Leu	Asp	Arg	Gly	Tyr	Ile	Ser	Pro	Tyr	Phe	Ile	Thr	Asn		
225					230					235					240		
Ser	Lys	Ala	Gln	Lys	Cys	Glu	Pro	Glu	Asp	Pro	Leu	Ile	Leu	Ile	His		
			245						250				255				
Asp	Arg	Lys	Val	Thr	Asn	Met	His	Ala	Val	Val	Lys	Val	Leu	Glu	Met		
			260					265					270				
Ala	Leu	Lys	Lys	Gln	Arg	Pro	Leu	Leu	Ile	Val	Ala	Glu	Asp	Val	Glu		
		275					280					285					
Ser	Glu	Ala	Leu	Gly	Thr	Leu	Ile	Ile	Asn	Lys	Leu	Arg	Ala	Gly	Ile		
	290					295					300						
Lys	Val	Cys	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Glu	Asn	Arg	Lys	Ala		
305					310					315					320		

Asn	Leu	Gln	Asp	Leu	Ala	Ile	Leu	Thr	Gly	Gly	Glu	Val	Ile	Thr	Glu	325	330	335
Glu	Leu	Gly	Met	Asn	Leu	Glu	Asn	Val	Glu	Pro	His	Met	Leu	Gly	Ser	340	345	350
Cys	Lys	Lys	Val	Thr	Val	Ser	Lys	Asp	Asp	Thr	Val	Ile	Leu	Asp	Gly	355	360	365
Ala	Gly	Asp	Lys	Lys	Ser	Ile	Glu	Glu	Arg	Ala	Asp	Gln	Ile	Arg	Ser	370	375	380
Ala	Val	Glu	Asn	Ser	Thr	Ser	Asp	Tyr	Asp	Lys	Glu	Lys	Leu	Gln	Glu	385	390	395
Arg	Leu	Ala	Lys	Leu	Ser	Gly	Gly	Val	Ala	Val	Leu	Lys	Ile	Gly	Gly	405	410	415
Ala	Ser	Glu	Ala	Glu	Val	Gly	Glu	Lys	Lys	Asp	Arg	Val	Thr	Asp	Ala	420	425	430
Leu	Asn	Ala	Thr	Lys	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Pro	Gly	Gly	435	440	445
Gly	Val	Ala	Leu	Leu	Tyr	Ala	Ser	Lys	Glu	Leu	Asp	Lys	Leu	Gln	Thr	450	455	460
Ala	Asn	Phe	Asp	Gln	Lys	Ile	Gly	Val	Gln	Ile	Ile	Gln	Asn	Ala	Leu	465	470	475
Lys	Thr	Pro	Val	His	Thr	Ile	Ala	Ser	Asn	Ala	Gly	Val	Glu	Gly	Ala	485	490	495
Val	Val	Val	Gly	Lys	Leu	Leu	Glu	Gln	Gly	Asn	Thr	Asp	Leu	Gly	Tyr	500	505	510
Asp	Ala	Ala	Lys	Asp	Glu	Tyr	Val	Asp	Met	Val	Lys	Ala	Gly	Ile	Ile	515	520	525
Asp	Pro	Leu	Lys	Val	Ile	Arg	Thr	Ala	Leu	Val	Asp	Ala	Ala	Ser	Val	530	535	540
Ser	Ser	Leu	Met	Thr	Thr	Thr	Glu	Ser	Ile	Ile	Val	Glu	Ile	Pro	Lys	545	550	555
Glu	Glu	Ala	Pro	Ala	Pro	Ala	Met	Gly	Gly	Met	Gly	Gly	Met	Asp	Tyr	565	570	575

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met	Ala	Ser	Thr	Asn	Ala	Leu	Ser	Ser	Thr	Ser	Ile	Leu	Arg	Ser	Pro	
1				5					10					15		
Thr	Asn	Gln	Ala	Gln	Thr	Ser	Leu	Ser	Lys	Lys	Val	Lys	Gln	His	Gly	
			20					25					30			
Arg	Val	Asn	Phe	Arg	Gln	Lys	Pro	Asn	Arg	Phe	Val	Val	Lys	Ala	Ala	
		35					40					45				
Ala	Lys	Asp	Ile	Ala	Phe	Asp	Gln	His	Ser	Arg	Ser	Ala	Met	Gln	Ala	
	50					55				60						
Gly	Ile	Asp	Lys	Leu	Ala	Asp	Ala	Val	Gly	Leu	Thr	Leu	Gly	Pro	Arg	
65				70					75					80		
Gly	Arg	Asn	Val	Val	Leu	Asp	Glu	Phe	Gly	Ser	Pro	Lys	Val	Val	Asn	
			85					90					95			
Asp	Gly	Val	Thr	Ile	Ala	Arg	Ala	Ile	Glu	Leu	Pro	Asp	Pro	Met	Glu	
		100						105					110			
Asn	Ala	Gly	Ala	Ala	Leu	Ile	Arg	Glu	Val	Ala	Ser	Lys	Thr	Asn	Asp	
		115					120					125				
Ser	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Ser	Ile	Leu	Ala	Arg	Glu	Ile	
		130				135					140					
Ile	Lys	Leu	Gly	Leu	Leu	Asn	Val	Thr	Ser	Gly	Ala	Asn	Pro	Val	Ser	
145				150						155				160		
Ile	Lys	Lys	Gly	Ile	Asp	Lys	Thr	Val	Ala	Ala	Leu	Val	Glu	Glu	Leu	
			165						170				175			
Glu	Lys	Leu	Ala	Arg	Pro	Val	Lys	Gly	Gly	Asp	Asp	Ile	Lys	Ala	Val	
		180						185					190			
Ala	Thr	Ile	Ser	Ala	Gly	Asn	Asp	Glu	Leu	Ile	Gly	Lys	Met	Ile	Ala	
		195					200					205				
Glu	Ala	Ile	Asp	Lys	Val	Gly	Pro	Asp	Gly	Val	Leu	Ser	Ile	Glu	Ser	
	210					215				220						
Ser	Asn	Ser	Phe	Glu	Thr	Thr	Val	Glu	Val	Glu	Glu	Gly	Met	Glu	Ile	
225				230						235				240		
Asp	Arg	Gly	Tyr	Ile	Ser	Pro	Gln	Phe	Val	Thr	Asn	Pro	Glu	Lys	Ser	
			245						250				255			
Ile	Val	Glu	Phe	Glu	Asn	Ala	Arg	Val	Leu	Ile	Thr	Asp	Gln	Lys	Ile	
		260					265						270			
Ser	Ala	Ile	Lys	Asp	Ile	Ile	Pro	Leu	Leu	Glu	Lys	Thr	Thr	Gln	Leu	

275					280					285					
Arg	Ala	Pro	Leu	Leu	Ile	Ile	Ser	Glu	Asp	Ile	Thr	Gly	Glu	Ala	Leu
290						295					300				
Ala	Thr	Leu	Val	Val	Asn	Lys	Leu	Arg	Gly	Ile	Leu	Asn	Val	Ala	Ala
305					310					315					320
Ile	Lys	Ala	Pro	Gly	Phe	Gly	Glu	Arg	Arg	Lys	Ala	Leu	Leu	Gln	Asp
				325					330					335	
Ile	Ala	Ile	Leu	Thr	Gly	Ala	Glu	Phe	Gln	Ala	Ser	Asp	Leu	Gly	Leu
			340					345					350		
Leu	Val	Glu	Asn	Thr	Thr	Ile	Glu	Gln	Leu	Gly	Leu	Ala	Arg	Lys	Val
		355					360					365			
Thr	Ile	Ser	Lys	Asp	Ser	Thr	Thr	Ile	Ile	Ala	Asp	Ala	Ala	Ser	Lys
	370					375					380				
Asp	Glu	Leu	Gln	Ser	Arg	Val	Ala	Gln	Leu	Lys	Lys	Glu	Leu	Ser	Glu
385					390					395					400
Thr	Asp	Ser	Ile	Tyr	Asp	Ser	Glu	Lys	Leu	Ala	Glu	Arg	Ile	Ala	Lys
				405					410					415	
Leu	Ser	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	Ala	Ala	Thr	Glu	Thr
			420					425					430		
Glu	Leu	Glu	Asp	Arg	Lys	Leu	Arg	Ile	Glu	Asp	Ala	Lys	Asn	Ala	Thr
		435					440					445			
Phe	Ala	Ala	Ile	Glu	Glu	Gly	Ile	Val	Pro	Gly	Gly	Gly	Thr	Ala	Leu
	450					455					460				
Val	His	Leu	Ser	Gly	Tyr	Val	Pro	Ala	Ile	Lys	Glu	Lys	Leu	Glu	Asp
465					470					475					480
Ala	Asp	Glu	Arg	Leu	Gly	Ala	Asp	Ile	Val	Gln	Lys	Ala	Leu	Val	Ala
				485					490					495	
Pro	Ala	Ala	Leu	Ile	Ala	Gln	Asn	Ala	Gly	Ile	Glu	Gly	Glu	Val	Val
			500					505					510		
Val	Glu	Lys	Ile	Lys	Asn	Gly	Glu	Trp	Glu	Val	Gly	Tyr	Asn	Ala	Met
		515					520					525			
Thr	Asp	Thr	Tyr	Glu	Asn	Leu	Val	Glu	Ser	Gly	Val	Ile	Asp	Pro	Ala
	530					535					540				
Lys	Val	Thr	Arg	Cys	Ala	Leu	Gln	Asn	Ala	Ala	Ser	Val	Ala	Gly	Met
545					550					555					560
Val	Leu	Thr	Thr	Gln	Ala	Ile	Val	Val	Glu	Lys	Pro	Lys	Pro	Lys	Ala
				565					570					575	
Ala	Val	Ala	Ala	Ala	Pro	Gln	Gly	Leu	Thr	Ile					
				580				585							



(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Ala	Lys	Asp	Ile	Lys	Phe	Gly	Glu	Glu	Ala	Arg	Arg	Ala	Met	Leu	
1				5					10					15		
Arg	Gly	Val	Asn	Ala	Leu	Ala	Asp	Ala	Val	Lys	Val	Thr	Leu	Gly	Pro	
			20					25					30			
Lys	Gly	Arg	Asn	Val	Val	Leu	Glu	Lys	Ser	Phe	Gly	Ala	Pro	Thr	Ile	
			35				40					45				
Thr	Lys	Asp	Gly	Val	Thr	Val	Ala	Lys	Glu	Ile	Glu	Leu	Glu	Asp	Lys	
			50				55				60					
Phe	Glu	Asn	Met	Gly	Ala	Gln	Leu	Val	Lys	Glu	Val	Ala	Ser	Lys	Thr	
65					70					75					80	
Asn	Asp	Val	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	Gln	
				85					90					95		
Ala	Ile	Val	Lys	Glu	Gly	Leu	Lys	Asn	Val	Ala	Ala	Gly	Ala	Asn	Pro	
			100					105					110			
Met	Asp	Leu	Arg	Arg	Gly	Ile	Asp	Lys	Ala	Val	Asp	Ala	Val	Val	Glu	
		115					120					125				
Glu	Leu	Lys	Ala	Ile	Ala	Lys	Pro	Val	Glu	Thr	Lys	Glu	Glu	Ile	Ala	
		130				135					140					
Gln	Val	Ala	Thr	Ile	Ser	Ala	Asn	Gly	Asp	Glu	Glu	Ile	Gly	Glu	Leu	
145					150					155					160	
Ile	Ala	Glu	Ala	Met	Glu	Lys	Val	Gly	Lys	Glu	Gly	Val	Ile	Thr	Val	
				165					170					175		
Glu	Glu	Gly	Lys	Thr	Leu	Glu	Thr	Glu	Leu	Glu	Val	Val	Glu	Gly	Met	
			180					185					190			
Gln	Phe	Asp	Arg	Gly	Tyr	Ile	Ser	Pro	Tyr	Phe	Ile	Thr	Asp	Ser	Glu	
			195				200					205				
Lys	Gln	Lys	Ala	Glu	Leu	Glu	Asp	Pro	Leu	Ile	Leu	Leu	Thr	Asp	Lys	
			210				215					220				
Lys	Ile	Ser	Asn	Ile	Gln	Asp	Leu	Leu	Pro	Val	Leu	Glu	Glu	Val	Ala	

225				230					235				240		
Gln	Ala	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	Glu
				245					250				255		
Ala	Leu	Ala	Thr	Leu	Val	Val	Asn	Lys	Leu	Arg	Gly	Thr	Leu	Lys	Val
				260					265				270		
Val	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Met	Leu
				275					280				285		
Gln	Asp	Ile	Ala	Ile	Leu	Thr	Gly	Gly	Gln	Val	Ile	Ser	Glu	Glu	Leu
				290					295				300		
Gly	Leu	Ser	Leu	Glu	Asp	Ala	Thr	Leu	Glu	Asp	Leu	Gly	Gln	Ala	Lys
				305					310				315		
Lys	Val	Val	Val	Thr	Lys	Asp	Asp	Thr	Thr	Ile	Val	Asp	Gly	Ala	Gly
				320					325				330		
Asp	Ala	Ala	Ile	Ala	Gly	Arg	Val	Ala	Gln	Ile	Arg	Ser	Gln	Ile	Glu
				335					340				345		
Glu	Ser	Thr	Ser	Asp	Tyr	Asp	Lys	Glu	Lys	Leu	Gln	Glu	Arg	Leu	Ala
				350					355				360		
Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	Ala	Ala	Thr	Glu
				365					370				375		
Val	Glu	Leu	Lys	Glu	Arg	Lys	Asp	Arg	Val	Glu	Asp	Ala	Leu	Asn	Ala
				380					385				390		
Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Pro	Gly	Gly	Gly	Val	Ala
				395					400				405		
Leu	Leu	Arg	Ala	Ala	Pro	Ala	Leu	Asp	Lys	Leu	Lys	Thr	Glu	Asn	Gly
				410					415				420		
Asp	Glu	Ala	Thr	Gly	Val	Asn	Ile	Val	Leu	Arg	Ala	Leu	Glu	Ala	Pro
				425					430				435		
Leu	Arg	Gln	Ile	Ala	Glu	Asn	Ala	Gly	Leu	Glu	Gly	Ser	Val	Val	Val
				440					445				450		
Glu	Lys	Val	Lys	Asn	Ser	Glu	Ala	Gly	Gly	Tyr	Asn	Ala	Ala	Thr	Gly
				455					460				465		
Glu	Tyr	Val	Asp	Met	Ile	Ala	Ala	Gly	Ile	Ile	Asp	Pro	Thr	Lys	Val
				470					475				480		
Thr	Arg	Ser	Ala	Leu	Gln	Asn	Ala	Ala	Ser	Val	Ala	Ser	Leu	Met	Leu
				485					490				495		
Thr	Thr	Glu	Ala	Val	Val	Val	Asp	Lys	Pro	Glu	Lys	Glu	Ala	Ala	Pro
				500					505				510		
Ala	Gly	Met	Pro	Gly	Met	Met	Gly	Gly	Met	Gly	Gly	Met	Gly	Gly	Met
				515					520				525		
				530					535				540		

Met  
545

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CATATGGCNG CNAAGAYGT AAAA

24

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TGATCACATC ATNCCNCCCA TNCC

24

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CATATGGCAA AAGAAATHAA RTTY

24

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TGATCANCCN CCCATNCCNC CCAT

24

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTAAAACGAC GGCCAG

16

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CAGGAAACAG CTATGAC

17

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCAACCATCA CGAAAGA

17

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACGGGTCACT TTGGTTG

17

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTACTAATGA CGGGGTA

17

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTACCAATGA CGGTGTG

17

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAGGGTCAA TGATTCC

17

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTGGATCAA TGATACC

17

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CCGTACCGTG CTCTGAC

17

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACCACGTTTC AGATCCA

17

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GACAGTTTCG CGGCAAC

17

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CTCAGAACGA AGATCAG

17

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGTATGCAGT TCGACCG

17

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CCGTGTTGGT CAAATCC

17

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGTAACTACG GTTACAA

17

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GAGGCCACTT CTTTCAC

17

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GGCTTCCAGC ACTGGCA

17

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

AACTTCAGTC GCAGCAC

17

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CCTTGAAAGC CATTGCT

17

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GCTACACGTG CAGCCGT

17

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCTGCAACAG GTGAGTG

17

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TCATGAACAA TGGCTTG

17

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACGAAGCACA ATGTTAC

17

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ATCACTAAAG ATGGTGT

17

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCAGTTGCCG CAGCAGT

17

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCTACTCGTG CAGCTGT

17

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GTTCTCCGTG CTTTGGA

17

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GCACCTGCTG TGACGTT

17

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TCTTCGATGG TGATGAC

17

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGCAAGAGCT GTTCCGC

17

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTGAGCCAGT ACGGTTG

17

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GTACTGCAGA GCGGAAC

17

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ACCGTCTTCA ACGGTGA

17

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GTTATCATTG CTGAAGA

17

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ACGGTACCGC CGGTCAG

17

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CTGGGCCAGG CTAAACG

17

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CGACTGAAGT TGAAATG

17

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GCTGTTGAAG AACTGAA

17

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GTCTTCAACG GTGATCA

17

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

TCTTCTACCG CAGCACG

17

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CTCTTGATTA TTGCGGA

17

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TTGTTCAAAA CAAGAGT

17

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CGATTATTGT AGAAGGT

17

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CTTGATAACC GCAACAC

17

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TCCAAAGCAC GGAGAAC

17

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GTGTCAAACA TCCAAGA

17

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TCTTCGATGG TAATCAC

17

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GCAATAATGA GTAATGG

17

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ACAGTAATTG TTGAAGG

17

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAGTGCAATA CGGTTAG

17

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AGCTTCCAGA ACCGGCA

17

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CTGATCATCG CTGAAGA

17

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ACGGTTATTG TAGAAG

16